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OM protein - protein search, using sw model

Run on: August 25, 2005, 11:30:48 ; Search time 165 Seconds

(without alignments)
35.160 Million cell updates/sec

Title: US-10-803-541-2

Perfect score: 81

Sequence: 1 LLGNSSPRTQSPQNC 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A Geneseq 16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	515	2	Aaw54236 Human Lam
2	81	100.0	515	4	Aab90770 Human ehe
3	81	100.0	664	6	Abu04992 Human exp
4	81	100.0	664	7	Ade63975 Human pro
5	81	100.0	664	7	Adj70273 Human hea
6	81	100.0	664	8	Adoi13765 Human wil
7	73	90.1	665	7	Adec3973 Rat Prote
8	48	59.3	172	8	Adrl0031 Human pro
9	46	56.8	103	4	Aam82436 Human inn
10	44	54.3	83	4	Abg22832 Novel hum
11	44	54.3	286	5	Abp43855 Mouse put
12	44	54.3	286	6	Ada55294 Human pro
13	44	54.3	443	4	Abb63545 Drosophil
14	44	54.3	970	6	Abrr53403 Protein s
15	44	54.3	970	7	Adk64724 Disease c
16	43	53.1	154	4	Aau52369 Propionib
17	43	53.1	154	6	Abm48888 Propionib
18	43	53.1	558	7	Adc08125 Rice prot
19	42	51.9	60	4	Aam88380 Human inn
20	42	51.9	105	2	Aaw61569 Vpr prote
21	42	51.9	105	2	Aam68196
22	42	51.9	129	3	Aagi10484 Arabidops
23	42	51.9	144	3	Aagi10483 Arabidops
24	42	51.9	164	7	Abos1750 Pseudomon
25	42	51.9	177	2	Aaw00642 Infectiou

26	42	51.9	177	2	Aaw06794
27	42	51.9	256	7	ADB65101
28	42	51.9	613	3	Aag42554 Arabidops
29	42	51.9	684	3	Aag42553 Arabidops
30	42	51.9	690	4	Abb71234 Drosophil
31	42	51.9	735	4	Abg06831 Novel hum
32	42	51.9	735	7	ADC33376
33	42	51.9	772	3	AAG42552 Arabidops
34	42	51.9	772	6	ADO61607 Transcrip
35	42	51.9	1224	8	ABR55649 Amino aci
36	42	51.9	2150	5	AAO22566 Wooden le
37	41	50.6	10	2	AAR15781 Farnesyl-
38	41	50.6	10	2	AAR49742 Farnesyl-
39	41	50.6	10	2	AAR77804 Farnesyl
40	41	50.6	10	2	Aaw04434 Farnesyl
41	41	50.6	68	4	AAU53546 Propionib
42	41	50.6	68	6	ABM50065
43	41	50.6	539	7	ADL06330
44	41	50.6	542	2	AAW26130
45	41	50.6	747	8	ADR86215
46	41	50.6	791	8	ADQ66060 Novel hum
47	41	50.6	871	8	ADK52121 Human ato
48	41	50.6	871	8	ADR09093 Human pro
49	41	50.6	1937	4	ABE58985 Drosophil
50	40	49.4	71	4	ABG20384 Novel hum
51	40	49.4	82	4	AAU61331 Propionib
52	40	49.4	82	6	ABM57850 Propionib
53	40	49.4	105	6	AAU66847 Propionib
54	40	49.4	105	6	ABM63366 Propionib
55	40	49.4	141	4	AAAM6096 Human inn
56	40	49.4	170	7	ADM05956 Human pro
57	40	49.4	172	4	AAU55863 Propionib
58	40	49.4	172	6	ABM52382 Propionib
59	40	49.4	234	7	ADM04835 Human pro
60	40	49.4	452	4	ABB71874 Drosophil
61	40	49.4	462	4	AAU93757 Human pro
62	40	49.4	462	4	AAU95328 Human pro
63	40	49.4	583	4	AAAM0015 Human pol
64	40	49.4	583	3	AAAB29657 Human mem
65	40	49.4	599	3	ABJ69809 Human hea
66	40	49.4	713	7	ABM68367 Photorhab
67	40	49.4	759	6	ADJ70343 Human hea
68	40	49.4	828	7	ABR41949 Rat ATPaa
69	40	49.4	1020	6	ADO28693 Human Na/
70	40	49.4	1020	8	ADQ28693 Human Na/
71	40	49.4	1054	8	ABO85034 Human can
72	40	49.4	1054	8	ABO85034 Human can
73	40	49.4	2063	8	ABO85033 Murine ca
74	40	49.4	2063	8	ABO85033 Murine ca
75	39.5	48.8	130	2	AAU21425 Human hig
76	39.5	48.8	5877	6	AAE34702 Human muc
77	39.5	48.8	10431	6	ABU54861 Human CA1
78	39.5	48.8	22152	8	ADP72871 Human ova
79	39.5	48.8	22157	8	ADP84155 Human CA1
80	39	48.1	45	8	ABO56724 Human gen
81	39	48.1	57	4	AAU66292 Propionib
82	39	48.1	57	4	AAU46738 Propionib
83	39	48.1	57	6	ABM62811 Propionib
84	39	48.1	57	6	ABM43257 Propionib
85	39	48.1	81	5	ABP04444 Human ORF
86	39	48.1	105	5	ABP03018 Human ORF
87	39	48.1	110	7	ADP74902 Human NOV
88	39	48.1	114	5	ABP70134 Human NOV
89	39	48.1	144	7	ABO77040 Pseudomon
90	39	48.1	178	6	ABM62278 Propionib
91	39	48.1	178	6	ABM58797 Propionib
92	39	48.1	267	3	AAU70223 Human RNA
93	39	48.1	267	4	AAU70223 Human RNA
94	39	48.1	281	2	ABR93544 Human pro
95	39	48.1	341	7	ADP71244 Human col
96	39	48.1	362	8	ADM90921 Human pha
97	39	48.1	385	5	ABP41904 Human ova
98	39	48.1	399	2	AAAR23846 Prepro fo

99 39 48.1 402 2 AAR27291 Human ost
100 39 48.1 402 2 AAR44759 Human ost

ALIGNMENTS

RESULT 1
AAW54236
ID AAW54236 standard; peptide; 515 AA.

AC AAW54236;
XX
XX 10-AUG-1998 (first entry)
XX Human Lamin A protein.
DE
XX Cervical cancer-associated protein; Cvc; tryptic peptide; human;
XX detection; treatment; Lamin A; non-chromatin protein.
XX
OS Homo sapiens.
XX
XX WO9809170-A2.
XX
XX 05-MAR-1998.
XX
XX 19-AUG-1997; 97WO-US014526.
XX
XX 30-AUG-1996; 96US-00705660.
XX
XX (MATR-) MATRITECH INC.
XX
XX Keese SK, Obar R, Wu Y;
PI
XX WPI; 1998-230271/20.
DR
XX
XX Detection and therapy of cervical cancer - using specific cervical cancer
XX -associated proteins as targets for treatment or as indicators for
PT detection.
XX

PS Claim 18; Page 68-69; 79pp; English.

XX This protein is the human lamin A which is used to obtain tryptic
XX peptides which are used in a method for detecting cervical cancer. The
XX method involves detecting the presence of a cervical cancer-associated
XX protein (Cvc) in a tissue or body fluid sample. The Cvc is characterised
XX as having a molecular weight of 4900-69400 Daltons as determined by
XX sodium dodecyl-sulphate (SDS)-PAGE techniques and an isoelectric point
XX (pI) of 5.1-6.6 as determined by standard isoelectric focusing
XX techniques. The protein is further characterised as being a non-chromatin
XX protein which is detectable at a higher level in a human cervical cancer
XX cell than in a normal human cervical cell, as determined by 2D-gel
XX electrophoresis. The methods can be used for the early and rapid
XX detection of cervical cancer, for treating cervical cancers and for
XX monitoring the efficacy of such treatment
XX

SQ Sequence 515 AA;

Query Match 100.0%; Score 81; DB 2; Length 515;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSPQNC 15
| | | | | | | | | | | | | | | | | |
Db 498 LLGNSSPRTQSPQNC 512

RESULT 2
AAB90770
ID AAB90770 standard; protein; 515 AA.

XX
XX AAB90770;
AC
XX

DT 15-JUN-2001 (first entry)
XX Human shear stress-response protein SEQ ID NO: 40.
DE
XX Human; shear stress-response protein; vascular disease; arteriosclerosis.
XX Homo sapiens.
XX WO200125427-A1.
XX 12-APR-2001.
XX 02-OCT-2000; 2000WO-JP006840.
XX 01-OCT-1999; 99JP-00280976.
XX (KYOWA) KYOWA HAKKO KOGYO KK.
XX (NOJI/) NOJIMA H.
XX Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;
PI Kuga T, Sekine S, Nakamura Y, Sugano S;
PI
XX WPI; 2001-266308/27.
XX N-PSDB; AAH02893.
XX DNA sequences, proteins encoded by them and antibodies against them
XX useful in diagnosis and treatment of vascular disease caused by
XX arteriosclerosis.
XX
XX Claim 60; Page 293-296; 678pp; Japanese.
XX
XX The present invention provides the protein and coding sequences of a
XX number of human shear stress response proteins. These are useful in the
XX diagnosis, treatment and screening of vascular diseases caused by
XX arteriosclerosis, including heart failure, post-PTCA restenosis and
XX hypertension
XX
XX Sequence 515 AA;

Query Match 100.0%; Score 81; DB 4; Length 515;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSPQNC 15
| | | | | | | | | | | | | | | | | |
Db 498 LLGNSSPRTQSPQNC 512

RESULT 3
ABU04992
ID ABU04992 standard; protein; 664 AA.

XX
XX AC
XX ABU04992;
XX
XX 29-JAN-2003 (first entry)
XX

DE Human expressed protein tag (EPT) #1658.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.
XX OS
XX WO200278524-A2.
XX

PD 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

```

PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCOS INC.
XX
XX Chicz RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX Example 2; SEQ ID NO 1658; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (BPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 664 AA;
XX
XX Query Match 100.0%; Score 81; DB 6; Length 664;
XX Best Local Similarity 100.0%; Pred. No. 0.00015;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 LLGNSSPRTQSPQNC 15
DB 647 LLGNSSPRTQSPQNC 661
XX
XX RESULT 4
XX ADE63975
XX ID ADE63975 standard; protein; 664 AA.
XX
XX ADE63975;
XX AC
XX
XX 29-JAN-2004 (first entry)
XX
XX Human Protein P02545, SEQ ID NO 9921.
XX
XX Human; pain; neuronal tissue; gene therapy;
XX spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GERO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENBANK; P02545.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a human protein (shown in Table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 664 AA;
XX
XX Query Match 100.0%; Score 81; DB 7; Length 664;
XX Best Local Similarity 100.0%; Pred. No. 0.00015;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 LLGNSSPRTQSPQNC 15
DB 647 LLGNSSPRTQSPQNC 661
XX
XX RESULT 5
XX ADJ70273
XX ID ADJ70273 standard; protein; 664 AA.
XX
XX ADJ70273;
XX AC
XX
XX 06-MAY-2004 (first entry)
XX
XX Human heat mitochondrial protein as a therapeutic target SeqID2079.
XX
XX mitochondrial; human; screening assay; diabetes mellitus;
XX Huntington's disease; osteoarthritis;
XX Leber's hereditary optic neuropathy; LHON;
XX mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
XX myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
XX neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
XX osteopathic; ophthalmological; cytostatic.
XX
XX Homo sapiens.
XX
XX OS
XX XX

```


CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention
 XX
 XX Sequence 103 AA;
 SQ Query Match 56.8%; Score 46; DB 4; Length 103;
 Best Local Similarity 57.1%; Pred. No. 13;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Qy 2 LGNSPRTQSPQNC 15
 Db 71 LGSWTPNTQPPQRC 84
 RESULT 10
 ID ABG22832 standard; protein; 83 AA.
 XX
 AC ABG22832;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #22823.
 XX
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 KW Homo sapiens.
 XX
 OS WO200175067-A2.
 XX
 PN 11-OCT-2001.
 XX
 PD 30-MAR-2001; 2001WO-US008631.
 XX
 PF 31-MAR-2000; 2000US-00540217.
 XX
 PR 23-AUG-2000; 2000US-00649167.
 XX
 XX (HYSE-) HYSEQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 XX
 PI WPI; 2001-639362/73.
 XX
 DR N-PSDB; AAS87019.
 XX
 DR New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 XX Claim 20; SEQ ID NO 53191; 103pp; English.
 PS The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 83 AA;
 SQ Query Match 54.3%; Score 44; DB 4; Length 83;
 Best Local Similarity 80.0%; Pred. No. 21;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 NSSPRTQSPQ 13
 Db 4 NSSPRSQSPR 13
 RESULT 11
 ABP43855
 ID ABP43855 standard; protein; 286 AA.
 XX
 AC ABP43855;
 XX
 DT 26-FEB-2003 (first entry)
 XX
 DE Mouse putative protein #15.
 XX
 DE Neuroprotective; immunomodulator; cancer; cytostatic; anti-inflammatory;
 KW gene therapy; nutritional supplement; wound; burn; ulcer;
 KW Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis;
 KW autoimmune disorder; inflammation; vulnery.
 XX
 OS Mus musculus.
 XX
 PN WO200231111-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 11-OCT-2001; 2001WO-US027760.
 XX
 PR 12-OCT-2000; 2000US-00687527.
 XX
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
 XX
 DR WPI; 2002-426278/45.
 XX
 DR N-PSDB; ABQ61099.
 XX
 DR New polypeptides and their encoded proteins, useful as nutritional
 PT sources or supplements, or in gene therapy, particularly for treating
 PT wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
 PT inflammation.
 XX
 XX Claim 20; SEQ ID # 758; 357pp + Sequence Listing; English.
 PS The invention relates to 446 newly isolated polynucleotide sequences. The
 CC activity of polynucleotides of the invention may be described as,
 CC vulnery, neuroprotective, immunomodulator, cytostatic and anti-
 CC inflammatory. Compositions comprising nucleic acids of the invention are
 CC useful for treating a mammalian subject, or as nutritional sources or
 CC supplements. These are useful in gene therapy, particularly for treating
 CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
 CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or
 CC inflammation. The nucleic acids and polypeptides are also useful in
 CC diagnostic and research methods. The sequences given in records ABP43544-

CC ABP43989 represent polypeptides encoded by polynucleotides of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX SQ Sequence 286 AA;

Query Match 54.3%; Score 44; DB 5; Length 286;
 Best Local Similarity 80.0%; Pred. No. 81;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 SPRTQSPQNC 15
 |||||
 Db 71 SPRTQSPGCG 80

RESULT 12
 ADA55294
 ID ADA55294 standard; protein; 286 AA.

XX AC ADA55294;

XX DT 20-NOV-2003 (first entry)

XX DE Human protein, SEQ ID 2862.

XX OS Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
 KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
 KW inflammatory disease; osteoporosis; neurological disease.

XX OS Homo sapiens.

XX FN EP1293569-A2.

XX PD 19-MAR-2003.

XX PF 21-MAR-2002; 2002EP-00006586.

XX PR 14-SEP-2001; 2001JP-00328381.

XX PR 24-JAN-2002; 2002US-0350435P.

XX PA (HELI-) HELIX RES INST.

XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX DR WPI; 2003-395539/38.

XX DR N-PSDB; ADA53655.

XX PT New polynucleotides encoding full-length polypeptides, e.g. secretory
 PT and/or membrane proteins, useful for developing medicines for diseases in
 PT which the gene is involved, or as target molecules for gene therapy.

XX PS Claim 14; SEQ ID NO 2862; 205pp; English.

XX The present invention relates to novel human secretory or membrane
 CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
 CC ADA54071). The coding sequences are useful in the gene therapy of
 CC diseases caused by abnormalities of the proteins, e.g. cancer,
 CC inflammatory diseases, osteoporosis or neurological disease.

XX SQ Sequence 286 AA;

Query Match 54.3%; Score 44; DB 6; Length 286;
 Best Local Similarity 80.0%; Pred. No. 81;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 SPRTQSPQNC 15
 |||||
 Db 71 SPRTQSPGCG 80

RESULT 13

ABR53403
 ID ABR53403 standard; protein; 443 AA.

XX AC ABR53403;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 17427.

XX KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.

XX PR 11-JUL-2000; 2000US-00614150.

XX PA (PEKE) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX DR WPI; 2001-656860/75.

XX DR N-PSDB; ABL07648.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.

XX PS Disclosure; SEQ ID NO 17427; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABR57737-
 CC ABR72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 443 AA;

Query Match 54.3%; Score 44; DB 4; Length 443;
 Best Local Similarity 64.3%; Pred. No. 1.3e+02;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSPON 14
 |||||

Db 397 LLONTSMRSQSPNN 410

RESULT 14

ABR53403
 ID ABR53403 standard; protein; 970 AA.

XX AC ABR53403;

XX DT 20-JUN-2003 (first entry)

XX DE Protein sequence #SEQ ID 1671.

XX KW Multiprotein complex; eukaryote; drug target; diagnosis.

XX OS Saccharomyces cerevisiae.

XX EP1258494-A1.
 XX 20-NOV-2002.
 XX 20-DEC-2001; 2001EP-00130253.
 XX 15-MAY-2001; 2001EP-00111774.
 XX (CELL-) CELLZONE AG.
 XX Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;
 PI Marzioch M, Schultz JD, Superti-Furga GD;
 XX WPI; 2003-250078/25.
 DR N-P5DB; ACC61445.
 XX New isolated protein complexes useful for diagnosing a disease or
 PT disorder, or as a target for an active agent of a pharmaceutical,
 PT preferably a drug target in the treatment or prevention of disease or
 PT disorder.
 XX Disclosure; SEQ ID NO 1671; 17pp + Sequence Listing; English.
 XX The invention relates to multiprotein complexes from eukaryotes. Proteins
 CC of the invention and DNA sequences encoding them are given in records
 CC ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are
 CC obtainable by using a protein as a bait and isolating the set of proteins
 CC which is attached thereto from cells. Such protein complexes may comprise
 CC up to 30 distinct proteins. Protein complexes of the invention are useful
 CC for diagnosing a disease or disorder, or as a target for an active agent
 CC of a pharmaceutical, preferably a drug target in the treatment or
 CC prevention of a disease or disorder. Note: The sequence data for this
 CC patent is not represented in the printed specification, but is based on
 CC sequence information supplied by the European Patent Office. The complete
 CC document is available on CD-ROM
 XX Sequence 970 AA;
 SQ
 Query Match 54.3%; Score 44; DB 6; Length 970;
 Best Local Similarity 75.0%; Pred. No. 3e+02;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 GNSSPRTQSPON 14
 DB 595 GKSSPSTQSKQN 606
 RESULT 15
 ADK64724
 ID ADK64724 standard; protein; 970 AA.
 XX AC ADK64724;
 XX 06-MAY-2004 (first entry)
 DT Disease treating protein complex-derived protein #1013.
 XX protein complex; drug target; diagnosis.
 XX Unidentified.
 XX EP1338608-A2.
 XX 27-AUG-2003.
 XX 20-DEC-2002; 2002EP-00102902.
 XX 20-DEC-2001; 2001EP-00130253.
 XX (CELL-) CELLZONE AG.
 XX Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;
 PI

PI Marzioch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;
 PI Michon A, Leutwein C, Rick J;
 XX WPI; 2003-638460/61.
 DR N-P5DB; ADK64725.
 XX New proteins and protein complexes from eukaryotes, useful as targets in
 PT drug screening, or in diagnosing or screening for the presence of a
 PT disease or disorder, or a predisposition for developing a disease or
 PT disorder in a subject.
 XX Disclosure; SEQ ID NO 2025; 13pp; English.
 XX The invention relates to novel protein complexes comprising a first and a
 CC second protein, or its derivative, fragment, homologue or variant. The
 CC proteins are selected from given protein complexes, which are not defined
 CC in the specification. The variants are encoded by nucleic acids that
 CC hybridize to the nucleic acids encoding the proteins under low stringency
 CC conditions. The protein complexes are useful as targets for an active
 CC agent of a pharmaceutical. These protein complexes are particularly
 CC useful as drugs targets for the treatment or preventing of a disease or
 CC disorder. The complexes and methods above are useful in diagnosing or
 CC screening for the presence of a disease or disorder or a predisposition
 CC for developing a disease or disorder in a subject. These are also useful
 CC in screening for a drug for treatment or prevention of a disease or
 CC disorder. The molecule that modulates the amount, activity or protein
 CC components of the complex is useful for the manufacture of a medicament
 CC for the treatment or prevention of a disease or disorder. This sequence
 CC corresponds to a protein of the invention. (Note: the sequence data for
 CC this patent did not form part of the printed specification but was
 CC obtained from the EPO in electronic format).
 XX Sequence 970 AA;
 SQ
 Query Match 54.3%; Score 44; DB 7; Length 970;
 Best Local Similarity 75.0%; Pred. No. 3e+02;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 GNSSPRTQSPON 14
 DB 595 GKSSPSTQSKQN 606
 RESULT 16
 AAU52369
 ID AAU52369 standard; protein; 154 AA.
 XX AC AAU52369;
 XX 27-FEB-2002 (first entry)
 DT Propionibacterium acnes immunogenic protein #13265.
 XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX Propionibacterium acnes.
 XX WO200181581-A2.
 XX 01-NOV-2001.
 XX 20-APR-2001; 2001WO-US012865.
 XX 21-APR-2000; 2000US-0199047P.
 PR 02-JUN-2000; 2000US-0208841P.
 PR 07-JUL-2000; 2000US-0216747P.
 XX (CORI-) CORIXA CORP.
 XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI

PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 01-DEC-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI, 2001-483426/52.
XX N-PSDB; AAK61161.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Claim 11; SEQ ID NO 15973; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased

CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX
XX SQ Sequence 60 AA;

XX Query Match 51.9%; Score 42; DB 4; Length 60;
XX Best Local Similarity 64.3%; Pred. No. 32;
XX Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

XX 1 LLGNSSPRTSQPN 14
XX |||:|||||
XX 34 LLGSSSPSTSVSQN 47

XX RESULT 20
XX AAW61569
XX ID AAW61569 standard; peptide; 105 AA.
XX AC AAW61569;
XX XX
XX DT 27-OCT-1998 (first entry)
XX XX
XX DE Vpr protein binding B29-1 amino acid sequence.
XX XX
XX KW Lentiviral infection; Vpr protein; HIV infection; cell stasis;
XX KW cell death.
XX OS Homo sapiens.
XX XX
XX EN W09835234-A1.
XX XX
XX PD 13-AUG-1998.
XX XX
XX PF 11-FEB-1998; 98WO-US003008.
XX XX
XX PR 11-FEB-1997; 97US-00797907.
XX XX
XX PA (REGC) UNIV CALIFORNIA.
XX XX
XX PI Chen ISY, Jowett JBM, Withers-Ward E;
XX XX
XX DR WPI, 1998-447375/38.
XX XX
XX PT Identification of compounds binding the HIV-1 Vpr protein - that block
XX PT Vpr-mediated cell stasis, useful for treating HIV-1 or other lentiviral
XX PT infections.
XX XX
XX PS Disclosure; Fig 8; 63pp; English.
XX XX
XX CC This represents the amino acid sequence of the B29-1 protein. This
XX CC protein can bind to the Vpr protein encoded by the HIV genome. The
XX CC invention provides a method of identifying an agent for use in treating
XX CC lentiviral infections. The method comprises contacting a cellular target
XX CC of the agent to block interaction of the Vpr protein with the cellular
XX CC target, where an agent which blocks this interaction is an anti-
XX CC lentiviral agent. Alternatively, the agent contacts a cell expressing the
XX CC Vpr protein under conditions where the Vpr protein induces cell stasis in
XX CC the absence of the agent. Identification of the agent is then observed by
XX CC blockage of Vpr-induced cell stasis. The method allows the identification
XX CC of compounds that block Vpr-mediated cell stasis and ultimately cell
XX CC death. The compounds can thus be used in the treatment of HIV and other
XX CC lentiviral infections


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SQ Sequence 105 AA;
Query Match 51.9%; Score 42; DB 2; Length 105;
Best Local Similarity 80.0%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GNSSPRTQSP 12
DB 83 GNSSPHTASP 92

RESULT 21
AAW68196
ID AAW68196 standard; peptide; 105 AA.
XX
AC AAW68196;
XX
DT 25-MAR-2003 (revised)
DT 29-OCT-1998 (first entry)
XX
DE Vpr binding protein B29-1 amino acid sequence.
XX
KW Lentivirus; Vpr protein; HIV infection; cell stasis; cell death; cancer;
KW autoimmune disease; B29-1.
XX
OS Homo sapiens.
XX
PN WO9835032-A2.
XX
PD 13-AUG-1998.
XX
PF 11-FEB-1998; 98WO-US003390.
XX
PR 11-FEB-1997; 97US-00798597.
XX
PR 24-OCT-1997; 97US-00959279.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Chen ISY, Jowett JEM, Withers-Ward E, Stewart SA, Poon B;
PI Feigon J, Dieckmann T;
XX
DR WPI; 1998-447229/38.
XX
PT Arresting cell growth using lentivirus Vpr virion protein - used for
PT treatment of cancer and screening for agents that reduce Vpr binding,
PT e.g. anti-HIV agents.
XX
PS Disclosure; Fig 7; 71pp; English.
XX
CC This represents the amino acid sequence of the B29-1 protein. This
CC protein can bind to the Vpr protein encoded by the HIV genome. This is
CC used as a cellular target in the method of the invention of identifying
CC antitumour therapeutic candidates. The invention provides a method for
CC arresting the growth of a cell by treatment with a Vpr lentivirus protein
CC or its analogue. Agents that reduce binding of Vpr to a cellular target
CC are useful for treating HIV (human immune deficiency virus) infection or
CC more generally for restoring growth. The antitumour agent identified is
CC useful for treating any type of cancer, since it induces cell stasis
CC (blocks development at the G2 stage) and death. The agents can also be
CC used for treating autoimmune diseases. (Updated on 25-MAR-2003 to correct
CC PI field.)
XX
SQ Sequence 105 AA;
Query Match 51.9%; Score 42; DB 2; Length 105;
Best Local Similarity 80.0%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GNSSPRTQSP 12
DB 83 GNSSPHTASP 92

RESULT 22
AAG10484
ID AAG10484 standard; protein; 129 AA.
XX
AC AAG10484;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8826.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
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PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
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PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147415P.
PR 09-AUG-1999; 99US-0147493P.
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PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
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PR 20-AUG-1999; 99US-0149723P.

PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
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PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
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PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 51.9%; Score 42; DB 3; Length 129;
Best Local Similarity 61.5%; Pred. No. 74;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LGNSSPRTQSPQN 14
|||||:|:|:|
Db 24 LGNSAPISSSPPN 36

RESULT 23
RAG10483
ID AAG10483 standard; protein; 144 AA.
XX AAG10483; AC
XX AAG10483; AC
DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 8825.
DE
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132484P.
PR 06-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
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PR 11-MAY-1999; 99US-0132565P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0137828P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
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PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
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PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
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PR 28-JUN-1999; 99US-0140655P.
PR 29-JUN-1999; 99US-0140823P.
PR 30-JUN-1999; 99US-0140991P.
PR 01-JUL-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 02-JUL-1999; 99US-0142154P.
PR 06-JUL-1999; 99US-0142350P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
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PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
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PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144844P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
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PR 27-AUG-1999; 99US-0151066P.

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PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
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PR 23-SEP-1999; 99US-0155486P.
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PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
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PR 07-OCT-1999; 99US-0158023P.
PR 08-OCT-1999; 99US-0158222P.
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PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 51.9%; Score 42; DB 3; Length 144;
Best Local Similarity 61.5%; Pred. No. 83;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LGNSPRTQSPQN 14
DB 39 LGNSAPISSSPPN 51

RESULT 24
ABO81750
ID ABO81750 standard; protein; 164 AA.
AC ABO81750;
XX
XX 29-JUL-2004 (first entry)
DT
DE Pseudomonas aeruginosa polypeptide #13925.
XX
XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
XX Pseudomonas aeruginosa.
OS
XX

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PN US6551795-B1.
XX
PD 22-APR-2003.
XX
XX 18-FEB-1999; 99US-00252991.
XX
XX 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX WPI; 2003-615309/58.
XX N-PSDB; ABD15321.
XX
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX useful as molecular targets for diagnostics, prophylaxis and treatment of
XX pathological conditions resulting from bacterial infection.
XX
XX Disclosure; SEQ ID NO 30496; 455pp; English.
XX
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
XX polynucleotides encoding them. The sequences are useful in diagnosis and
XX therapy of pathological conditions, as molecular targets for diagnostics,
XX prophylaxis and treatment of pathological conditions resulting from a
XX bacterial infection, for evaluating a compound, such as a polypeptide,
XX for the ability to bind a P. aeruginosa nucleic acid, as components of
XX effective antibacterial targets, as targets for antibacterial drugs,
XX including anti-P. aeruginosa drugs, as templates for recombinant
XX production of P. aeruginosa-derived peptides or polypeptides, as target
XX components for diagnosis and/or treatment of P. aeruginosa-caused
XX infection, and in detection of P. aeruginosa sequences or other sequences
XX of Pseudomonas species using biochip technology. Sequences ABO67826-
XX ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
XX sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html
XX
XX Sequence 164 AA;

Query Match 51.9%; Score 42; DB 7; Length 164;
Best Local Similarity 63.6%; Pred. No. 96;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SSPRTQSPQMC 15
DB 22 SNPRHQEPQSC 32

RESULT 25
AAW00642
ID AAW00642 standard; protein; 177 AA.
XX
XX AAW00642;
XX
XX 16-OCT-2003 (revised)
DT 19-NOV-1996 (first entry)
XX
XX Infectious laryngotracheitis virus ORF8 RC product.
XX
XX Infectious laryngotracheitis virus; ILTV; herpesvirus; attenuation;
XX vector; vaccine; chicken; poultry; immunisation.
XX
XX Gallid herpesvirus 1.
XX OS
XX WO9508622-A1.
XX
XX 30-MAR-1995.
PD
XX
XX 16-SEP-1994; 94WO-US010628.
XX
XX 24-SEP-1993; 93US-00126597.
XX

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XX (SYTR ) SYNTRO CORP.
PA
XX Wild MA, Cochran MD;
PI
XX WPI; 1995-139591/18.
DR
XX N-PSDB; AAT33513.
DR
XX
XX Recombinant attenuated infectious laryngotracheitis virus - for use in
PT vaccines to protect poultry from infection from the virus, also methods
PT of distinguishing between vaccinated and naturally infected birds.
XX
XX Example 1; Page 116-117; 177pp; English.
XX
XX A protein (AAW06794) of unknown function is the product of the ORF8
CC reverse complement gene (AAT33513) transcribed from bases 11,150-10,617
CC on the reverse complement strand of the unique short region (see also
CC AAT33504) of infectious laryngotracheitis virus (ILT) genomic DNA. The
CC protein has a mol.wt. of approx. 19,470. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 177 AA;
XX
XX Query Match 51.9%; Score 42; DB 2; Length 177;
XX Best Local Similarity 53.3%; Pred. No. 1e+02;
XX Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
XX
XX 1 LLGNSSPRTQSPQNC 15
XX || ||| |||
XX 5 LLNRGSPRLNSPPKC 19
XX
XX RESULT 26
XX ID AAW06794 standard; protein; 177 AA.
XX AC AAW06794;
XX
XX 16-OCT-2003 (revised)
XX 02-JUN-1997 (first entry)
XX
XX ILTV unique short region ORF8 (reverse complement) product.
XX
XX ILTV; vaccine; vector; attenuation; poultry;
XX avian infectious bronchitis virus; Newcastle disease virus;
XX infectious bursal disease virus of chickens; Marek's disease virus;
XX herpesvirus.
XX
XX Gallid herpesvirus 1; USDA strain 8302.
XX
XX WO9629396-A1.
XX
XX 26-SEP-1996.
XX
XX 21-MAR-1996; 96WO-US003916.
XX
XX 23-MAR-1995; 95US-00410121.
XX 06-JUN-1995; 95US-00468190.
XX
XX (SYTR ) SYNTRO CORP.
XX
XX Wild MA, Cochran MD;
XX
XX WPI; 1996-443172/44.
XX N-PSDB; AAT44384, AAT44385.
XX
XX Recombinant infectious laryngotracheitis virus with deletion in the
PT glyco:protein G, GI or US2 gene, etc. - useful for vaccines against
PT infectious laryngotracheitis in poultry.
XX
XX Example 11; Page 125; 216pp; English.
XX
XX A 177-amino acid polypeptide (AAW06794) of unknown function is encoded by
CC

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CC open reading frame 8 (reverse complement) of the unique short region
CC (AAT44384) of infectious laryngotracheitis virus (ILT). Attenuated
CC recombinant ILTVs have at least one deletion in the unique short region
CC and can be used in vaccines against ILTV, and also in multivalent
CC vaccines for one or more avian diseases. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 177 AA;
XX
XX Query Match 51.9%; Score 42; DB 2; Length 177;
XX Best Local Similarity 53.3%; Pred. No. 1e+02;
XX Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
XX
XX 1 LLGNSSPRTQSPQNC 15
XX || ||| |||
XX 5 LLNRGSPRLNSPPKC 19
XX
XX RESULT 27
XX ID ADB65101 standard; protein; 256 AA.
XX AC ADB65101;
XX
XX 04-DEC-2003 (first entry)
XX
XX Human protein encoded by clone SPLEN20015100.
XX
XX Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
XX cell regeneration; membrane protein; signal transduction-related protein;
XX transcription-related protein; osteoporosis; neurological disease;
XX cancer; tumour.
XX
XX Homo sapiens.
XX
XX EP1308459-A2.
XX
XX 07-MAY-2003.
XX
XX 28-MAR-2002; 2002EP-00007401.
XX
XX 05-NOV-2001; 2001JP-00379298.
XX 25-JAN-2002; 2002US-00350978.
XX
XX (HELI-) HELIX RES INST.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
XX Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
XX Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
XX WPI; 2003-450961/43.
XX N-PSDB; ADB63131.
XX
XX New polynucleotides and polypeptides, useful for developing a diagnostic
XX marker or medicines for regulation of their expression and activity, or
XX as targets of gene therapy.
XX
XX Claim 1; Page; 222pp; English.
XX
XX The invention discloses a polynucleotide comprising a sequence selected
XX from 1970 fully defined nucleotide sequences which encode novel
XX polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
XX or its partial peptide, an antibody binding to the polypeptide or peptide
XX of the polynucleotide, immunologically assaying the polypeptide or
XX peptide of the polynucleotide by contacting the polypeptide or peptide
XX with the antibody of the encoded protein, and observing the binding
XX between the two, a transformant carrying the polynucleotide in an
XX expressible manner and an antisense polynucleotide. The oligonucleotide
XX is useful as a primer for synthesising the polynucleotide, or as a probe
XX for detecting the polynucleotide. The polynucleotides and encoded
XX proteins are useful as pharmaceutical agents and many disease-related
XX genes may be included in them, for developing a diagnostic marker or
XX

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CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a protein of the invention. Note: Some of the
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.

XX Sequence 256 AA;

Query Match 51.9%; Score 42; DB 7; Length 256;

Best Local Similarity 80.0%; Pred. NO. 1.5e+02;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GNSSPRTQSP 12

|||||

Db 234 GNSSPHTASP 243

RESULT 28

AAAG42554

ID AAAG42554 standard; protein; 613 AA.

XX AC AAAG42554;

XX 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 53084.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.

PR 28-APR-1999; 99US-0130891P.

PR 30-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132048P.

PR 04-MAY-1999; 99US-0132407P.

PR 05-MAY-1999; 99US-0132484P.

PR 06-MAY-1999; 99US-0132485P.

PR 06-MAY-1999; 99US-0132486P.

PR 07-MAY-1999; 99US-0132863P.

PR 11-MAY-1999; 99US-0132863P.

PR 14-MAY-1999; 99US-0134218P.

PR 14-MAY-1999; 99US-0134219P.

PR 14-MAY-1999; 99US-0134221P.

PR 14-MAY-1999; 99US-0134370P.

PR 18-MAY-1999; 99US-0134768P.

PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
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PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
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PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
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PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
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PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
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PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
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PR 21-JUL-1999; 99US-0145086P.
PR 22-JUL-1999; 99US-0145088P.
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PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
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PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
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PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
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PR 06-AUG-1999; 99US-0147303P.
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PR 12-AUG-1999; 99US-0148341P.
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PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
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PR 27-AUG-1999; 99US-0151065P.
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PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
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PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match 51.9%; Score 42; DB 3; Length 613;
Best Local Similarity 61.5%; Pred. No. 3.9e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LGNSPRTQSPQN 14
|||||: |||
Db 508 LGNSAPISSPPN 520

RESULT 29

AAG42553

ID AAG42553 standard; protein; 684 AA.

AC AAG42553;

XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 53083.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

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XX 25-MAR-1999; 99US-0126264P.

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XX 01-APR-1999; 99US-0127462P.

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XX 18-MAY-1999; 99US-0134768P.

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PR 04-AUG-1999;	99US-0147204P.	PR 29-OCT-1999;	99US-0162142P.
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Query Match 51.9%; Score 42; DB 3; Length 684;
 Best Local Similarity 61.5%; Pred. No. 4.4e+02;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LGNSSPRTQSPQN 14
 DB 579 LGNSAPISPPEN 591

RESULT 30
 ABB71234
 ID ABB71234 standard; protein; 690 AA.

XX AC ABB71234;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 40494.

XX KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.

XX PR 11-JUL-2000; 2000US-00614150.

XX PA (PEKE) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX DR WPI; 2001-656860/75.

XX DR N-PSDB; ABLI5337.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

XX PS Disclosure; SEQ ID NO 40494; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLI6176-ABLI30511), expressed DNA sequences (ABLI01840-ABLI6175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 690 AA;

Query Match 51.9%; Score 42; DB 4; Length 690;
 Best Local Similarity 50.0%; Pred. No. 4.5e+02;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 LGNSSPRTQSPQN 14
 DB 55 VIGNSLTSPAPQN 68

RESULT 31

ABG06831

ID ABG06831 standard; protein; 735 AA.

XX AC ABG06831;

XX 13-FEB-2002 (first entry)
 DT Novel human diagnostic protein #6822.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS71018.

XX PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

XX PS Claim 20; SEQ ID NO 37190; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 735 AA;

Query Match 51.9%; Score 42; DB 4; Length 735;
 Best Local Similarity 57.1%; Pred. No. 4.8e+02;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLGNSSPRTQSPQN 14

DB 129 LLGSPVPAQSPQS 142

RESULT 32

ADC33376

ID ADC33376 standard; protein; 735 AA.

XX AC ADC33376;

XX DT 18-DEC-2003 (first entry)

XX DE Human novel contig-encoded polypeptide sequence, SEQ ID NO:3458.
XX KW Human; diagnostic; drug screening; forensics; gene mapping;
XX KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;
XX KW neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
XX KW ulcers; osteoporosis; autoimmune disease; cancer;
XX KW molecular weight marker; food supplement; antiparkinsonian; nootropic;
XX KW neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
XX KW antilulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
XX KW gene therapy; chromosome 17.
XX OS Homo sapiens.
XX FN WO2003029271-A2.
XX PD 10-APR-2003.
XX PF 24-SEP-2002; 2002WO-US030474.
XX PR 24-SEP-2001; 2001US-0324631P.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
XX PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
XX PI Haley-Vicente D, Drmanac RT;
XX DR WPI; 2003-371981/35.
XX DR N-PSDB; ADC32609.
XX PT New polynucleotide and polypeptide useful for diagnosing, preventing or
XX PT treating conditions such as neurodegenerative diseases, anemias, platelet
XX PT disorders, wounds, ulcers, osteoporosis, autoimmune diseases or
XX PT cancer.
XX PS Example 2; SEQ ID NO 3458; 1185pp; English.
XX CC The invention relates to 971 novel human cDNA sequences (ADC29919-
XX CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
XX CC invention also relates to nucleic acid sequences over 99% identical with
XX CC the novel human cDNAs. The invention additionally encompasses expression
XX CC vectors and host cells comprising a nucleic acid of the invention; the
XX CC recombinant production of a polypeptide of the invention; an antibody
XX CC against a polypeptide of the invention; a method of detecting
XX CC polynucleotides or polypeptides of the invention; and methods of
XX CC identifying a compound which binds to a polypeptide of the invention. The
XX CC invention further discloses methods of preventing, treating or
XX CC ameliorating a medical condition; kits comprising polynucleotide probes
XX CC and/or monoclonal antibodies for carrying out the methods of the
XX CC invention; methods for the identification of compounds that modulate the
XX CC expression or activity of the polynucleotide and/or polypeptide; and 767
XX CC contig sequences corresponding to the cDNA sequences of the invention
XX CC (ADC31961-ADC32627) and the polypeptides encoded by the contigs (ADC32628
XX CC -ADC33394). The nucleic acids and polypeptides of the invention are
XX CC useful in diagnostics, drug screening, forensics, gene mapping, in the
XX CC identification of mutations responsible for genetic disorders or other
XX CC traits, for assessing biodiversity, and in producing many other types of
XX CC data and products dependent on DNA and amino acid sequences. They are
XX CC also used for treating diseases such as Parkinson's disease, Alzheimer's
XX CC disease and other neurodegenerative diseases, anaemia, platelet
XX CC disorders, wounds, ulcers, osteoporosis, autoimmune diseases or
XX CC cancer. The nucleic acids may also be used as hybridisation probes or
XX CC primers, and in the recombinant production of a protein. The polypeptides
XX CC are also useful in generating antibodies, as molecular weight markers,
XX CC and as food supplements. The present sequence represents a human contig-
XX CC encoded polypeptide sequence used in an example of the invention. Note:
XX CC The sequence data for this patent did not form part of the printed
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX CC Sequence 735 AA;

Query Match 51.9%; Score 42; DB 7; Length 735;
Best Local Similarity 57.1%; Pred. NO. 4.8e+02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 LLGNSSPRTQSPQN 14
Db 129 LLGSPVPQAQSPQS 142
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RESULT 33
AAG42552
ID AAG42552 standard; protein; 772 AA.
XX AC AAG42552;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 53082.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EF1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
XX PR 05-MAR-1999; 99US-0123180P.
XX PR 09-MAR-1999; 99US-0123548P.
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XX PR 29-MAR-1999; 99US-0126785P.
XX PR 01-APR-1999; 99US-0127462P.
XX PR 06-APR-1999; 99US-0128234P.
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XX PR 10-JUN-1999; 99US-0138847P.

PR	14-JUN-1999;	99US-0139119P.	PR	11-AUG-1999;	99US-0148319P.
PR	16-JUN-1999;	99US-0139452P.	PR	12-AUG-1999;	99US-0148341P.
PR	16-JUN-1999;	99US-0139453P.	PR	13-AUG-1999;	99US-0148565P.
PR	17-JUN-1999;	99US-0139453P.	PR	13-AUG-1999;	99US-0148684P.
PR	18-JUN-1999;	99US-0139454P.	PR	16-AUG-1999;	99US-0149358P.
PR	18-JUN-1999;	99US-0139455P.	PR	17-AUG-1999;	99US-0149175P.
PR	18-JUN-1999;	99US-0139456P.	PR	18-AUG-1999;	99US-0149426P.
PR	18-JUN-1999;	99US-0139457P.	PR	20-AUG-1999;	99US-0149722P.
PR	18-JUN-1999;	99US-0139458P.	PR	20-AUG-1999;	99US-0149723P.
PR	18-JUN-1999;	99US-0139459P.	PR	20-AUG-1999;	99US-0149929P.
PR	18-JUN-1999;	99US-0139460P.	PR	23-AUG-1999;	99US-0149902P.
PR	18-JUN-1999;	99US-0139461P.	PR	23-AUG-1999;	99US-0149930P.
PR	18-JUN-1999;	99US-0139462P.	PR	25-AUG-1999;	99US-0150566P.
PR	18-JUN-1999;	99US-0139463P.	PR	26-AUG-1999;	99US-0150884P.
PR	18-JUN-1999;	99US-0139464P.	PR	27-AUG-1999;	99US-0151065P.
PR	18-JUN-1999;	99US-0139750P.	PR	27-AUG-1999;	99US-0151066P.
PR	18-JUN-1999;	99US-0139763P.	PR	27-AUG-1999;	99US-0151080P.
PR	21-JUN-1999;	99US-0139817P.	PR	30-AUG-1999;	99US-0151303P.
PR	22-JUN-1999;	99US-0139899P.	PR	31-AUG-1999;	99US-0151388P.
PR	23-JUN-1999;	99US-0140353P.	PR	01-SEP-1999;	99US-0151930P.
PR	23-JUN-1999;	99US-0140354P.	PR	07-SEP-1999;	99US-0152363P.
PR	24-JUN-1999;	99US-0140698P.	PR	10-SEP-1999;	99US-0153070P.
PR	28-JUN-1999;	99US-0140823P.	PR	13-SEP-1999;	99US-0153758P.
PR	29-JUN-1999;	99US-0140991P.	PR	15-SEP-1999;	99US-0154018P.
PR	30-JUN-1999;	99US-0141287P.	PR	16-SEP-1999;	99US-0154039P.
PR	01-JUL-1999;	99US-0141842P.	PR	20-SEP-1999;	99US-0154779P.
PR	01-JUL-1999;	99US-0142154P.	PR	22-SEP-1999;	99US-0155139P.
PR	02-JUL-1999;	99US-0142058P.	PR	23-SEP-1999;	99US-0155486P.
PR	06-JUL-1999;	99US-0142390P.	PR	24-SEP-1999;	99US-0155659P.
PR	08-JUL-1999;	99US-0142803P.	PR	28-SEP-1999;	99US-0156458P.
PR	09-JUL-1999;	99US-0142920P.	PR	29-SEP-1999;	99US-0156596P.
PR	12-JUL-1999;	99US-0142977P.	PR	04-OCT-1999;	99US-0157117P.
PR	13-JUL-1999;	99US-0143542P.	PR	05-OCT-1999;	99US-0157753P.
PR	14-JUL-1999;	99US-0143624P.	PR	06-OCT-1999;	99US-0157865P.
PR	15-JUL-1999;	99US-0144005P.	PR	07-OCT-1999;	99US-0158029P.
PR	16-JUL-1999;	99US-0144085P.	PR	08-OCT-1999;	99US-0158232P.
PR	16-JUL-1999;	99US-0144086P.	PR	12-OCT-1999;	99US-0158369P.
PR	19-JUL-1999;	99US-0144325P.	PR	13-OCT-1999;	99US-0159293P.
PR	19-JUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159329P.
PR	19-JUL-1999;	99US-0144333P.	PR	14-OCT-1999;	99US-0159330P.
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159331P.
PR	19-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159637P.
PR	20-JUL-1999;	99US-0144352P.	PR	14-OCT-1999;	99US-0159638P.
PR	20-JUL-1999;	99US-0144632P.	PR	18-OCT-1999;	99US-0159584P.
PR	20-JUL-1999;	99US-0144884P.	PR	21-OCT-1999;	99US-0160741P.
PR	21-JUL-1999;	99US-0144814P.	PR	21-OCT-1999;	99US-0160767P.
PR	21-JUL-1999;	99US-0145086P.	PR	21-OCT-1999;	99US-0160768P.
PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160770P.
PR	22-JUL-1999;	99US-0145087P.	PR	21-OCT-1999;	99US-0160814P.
PR	22-JUL-1999;	99US-0145089P.	PR	21-OCT-1999;	99US-0160815P.
PR	22-JUL-1999;	99US-0145192P.	PR	21-OCT-1999;	99US-0160815P.
PR	23-JUL-1999;	99US-0145145P.	PR	22-OCT-1999;	99US-0160980P.
PR	23-JUL-1999;	99US-0145218P.	PR	22-OCT-1999;	99US-0160981P.
PR	23-JUL-1999;	99US-0145224P.	PR	22-OCT-1999;	99US-0160989P.
PR	23-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0161404P.
PR	26-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0161405P.
PR	27-JUL-1999;	99US-0145913P.	PR	25-OCT-1999;	99US-0161406P.
PR	27-JUL-1999;	99US-0145918P.	PR	26-OCT-1999;	99US-0161359P.
PR	27-JUL-1999;	99US-0145919P.	PR	26-OCT-1999;	99US-0161360P.
PR	28-JUL-1999;	99US-0145951P.	PR	26-OCT-1999;	99US-0161361P.
PR	02-AUG-1999;	99US-0146386P.	PR	28-OCT-1999;	99US-0161920P.
PR	02-AUG-1999;	99US-0146388P.	PR	28-OCT-1999;	99US-0161920P.
PR	02-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-0161992P.
PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161993P.
PR	04-AUG-1999;	99US-0147204P.	PR	29-OCT-1999;	99US-0162142P.
PR	04-AUG-1999;	99US-0147302P.			
PR	05-AUG-1999;	99US-0147192P.			
PR	05-AUG-1999;	99US-0147260P.			
PR	06-AUG-1999;	99US-0147303P.			
PR	06-AUG-1999;	99US-0147416P.			
PR	09-AUG-1999;	99US-0147493P.			
PR	09-AUG-1999;	99US-0147935P.			
PR	10-AUG-1999;	99US-0148171P.			

Query Match 51.9%; Score 42; DB 3; Length 772;
Best Local Similarity 61.5%; Pred. No. 5.1e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 LGNSPRTQSPQN 14
DB 667 LGNSAPISSPPN 679

RESULT 34
ADO61607
ID ADO61607 standard; protein; 772 AA.
XX
AC ADO61607;
DT 15-JUL-2004 (first entry)
XX
XX Transcription factor G324, SEQ ID 74.
DE
XX Plant; transcription factor; transgenic plant; abiotic stress tolerance;
KW osmotic stress tolerance; cold tolerance; heat tolerance;
KW low nitrogen tolerance; low phosphate tolerance; fungal disease;
KW glycosate resistance; flowering; fertility; seed development.
XX
OS Arabidopsis thaliana.
XX
XX WO2004031349-A2.
FN
XX 15-APR-2004.
XX
XX 18-SEP-2003; 2003WO-US030292.
XX
XX 18-SEP-2002; 2002US-0411837P.
PR 17-DEC-2002; 2002US-0434166P.
PR 24-APR-2003; 2003US-0465809P.
XX
XX (MEND-) MENDEL BIOTECHNOLOGY INC.
PA
XX Jiang C, Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL;
PI Riechmann JL, Haake V, Dubell AN, Keddle JS, Sherman BK;
XX
XX WPI; 2004-330163/30.
DR N-PSDB; ADO61606.
XX
XX New recombinant polynucleotide encoding transcription factor
PT polypeptides, useful for producing transgenic plants with advantageous
PT properties compared to a reference plant.
XX
XX Claim 16; SEQ ID NO 74; 510pp; English.
PS
XX The present invention relates to novel plant transcription factor
CC proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The
CC sequences can be used to produce transgenic plants, which overexpress
CC (II), where the transgenic plant has an altered trait as compared to a
CC non-transgenic plant or wild-type plant. The transgenic plant comprises
CC an altered trait selected from increased tolerance to abiotic stresses,
CC increased tolerance to osmotic stress, increased tolerance to cold,
CC germination in heat, increased tolerance to freezing conditions,
CC increased tolerance to low nitrogen conditions, increased tolerance to
CC low phosphate conditions, increased tolerance to disease, including
CC fungal disease and particularly Erysiphe, Fusarium and Botrytis,
CC increased tolerance to multiple fungal pathogens, increased resistance to
CC glycosate, increased sensitivity to ABA, reduced sensitivity to ABA,
CC increased sensitivity to ACC, altered sugar sensing, increased tolerance
CC to sugars, altered carbon/nitrogen sensing, early flowering, late
CC flowering, altered flower structure, loss of flower determinacy, reduced
CC fertility, altered shoot meristem development, altered branching pattern,
CC altered stem morphology, altered vascular tissue structure, reduced
CC apical dominance, altered trichome density, altered trichome development,
CC altered trichome structure, altered root development, altered shade
CC avoidance, altered seed development, altered seed ripening, altered seed
CC germination, slow growth, fast growth, altered cell differentiation,
CC altered cell proliferation, altered cell expansion, altered phase change,
CC altered senescence, abnormal embryo development, altered programmed cell
CC death, lethality when overexpressed, altered necrosis patterns, increased
CC plant size, increased biomass, large seedlings, dwarfed plants, dark
CC green leaves, change in leaf shape, increased leaf size and mass, light
CC green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,
CC altered seed coloration, altered seed size, altered seed shape, large

CC seed, increased leaf wax, increased leaf fatty acids, altered seed oil
CC content, altered seed protein content, altered seedprenyl content,
CC altered leaf prenyl lipid content, increased anthocyanin levels, and
CC decreased anthocyanin levels. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 772 AA;

Query Match 51.9%; Score 42; DB 8; Length 772;
Best Local Similarity 61.5%; Pred. No. 5.1e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LGNSPRTQSPQN 14
| | | | : | | |
Db 667 LGNSAPISPPN 679

RESULT 35

ABR55649
ID ABR55649 standard; peptide; 1224 AA.

XX AC ABR55649;

XX 11-AUG-2003 (first entry)

XX Amino acid of an open reading frame of the pyranosone dehydratase gene.

XX Pyranosone dehydratase; enzyme; microthecin; ascopyrone P; cortalcerone;
KW Aphanomyces; 2-furyl-hydroxymethyl-ketone; 2-furylglyoxal;
KW 4-deoxy-glycero-hexo-2,3-dilucose; plant protectant; seed protectant;
KW antimicrobial; antifungal.

XX Phanerochaete chrysosporium.

XX WO2003037918-A2.

XX 08-MAY-2003.

XX 30-OCT-2002; 2002WO-GB004916.

XX 31-OCT-2001; 2001GB-00026164.

XX 21-DEC-2001; 2001US-0343485P.

XX (DANI-) DANISCO AS.

XX Morgan AJ, Yu S, Weiergang I, Pedersen HC;

XX WPI; 2003-441351/41.

XX Novel polypeptide having pyranosone dehydratase activity, useful for
XX preparing microthecin, ascopyrone P or cortalcerone which are useful as
XX antimicrobial agents.

XX Disclosure; Fig 5; 96pp; English.

XX ABR55647-49 represent proteins encoded the open reading frames of the
XX pyranosone dehydratase gene. This enzyme is useful for preparing
XX microthecin, ascopyrone P (APP) or cortalcerone. Microthecin or
XX cortalcerone, or its derivatives or isomers, are useful in preventing
XX and/or inhibiting the growth of, and/or killing the pathogen Aphanomyces,
XX preferably A. cohioides. The derivative of microthecin is 2-furyl-
XX hydroxymethyl-ketone or 4-deoxy-glycero-hexo-2,3-dilucose. The derivative
XX of cortalcerone is 2-furylglyoxal. Microthecin or cortalcerone, or its
XX derivatives or isomers, are also useful for treating plant or plant seeds
XX (such as sugar beet seeds) or as a plant or seed protectant. Microthecin
XX and cortalcerone are useful as antimicrobial agents, particularly in food
XX stuffs. Microthecin is useful as an antifungal for plant protection

XX Sequence 1224 AA;

Query Match 51.9%; Score 42; DB 6; Length 1224;

Best Local Similarity 50.0%; Pred. No. 8.3e+02; DB 5; Length 2150; Mismatches 3; Conservative 7; Indels 0; Gaps 0;

Qy 2 LGNSPRTQSPQNC 15
:| ||| :| |||
Db 67 IGLASPITETQRC 80

RESULT 36
AAO22566
ID AAO22566 standard; protein; 2150 AA.
XX
AC AAO22566;
XX
DT 28-OCT-2002 (first entry)
XX
DE Wooden leg (WOL) gene related protein SEQ ID No 17.
XX
KW Wooden leg; WOL; vasculature; transgenic plant; agronomic; longer root;
KW wood production; plant; promoter; tree; crop plant.
XX
OS Arabidopsis thaliana.
XX
PN WO200244337-A2.
XX
PD 06-JUN-2002.
XX
PF 29-NOV-2001; 2001WO-US045053.
XX
PR 29-NOV-2000; 2000US-0253739P.
XX
PA (UUNY) UNIV NEW YORK STATE.
PA (HELA/) HELARIUTTA Y.
PA (MAHO/) MAHONEN A P.
PA (BONK/) BONKE A W M.
PA (KAUP/) KAUPPINEN L.
PA (RIIK/) RIIKONEN M.
XX
PI Helariutta Y, Mahonen AP, Bonke AWM, Kauppinen L, Riikonen M;
PI Benfey PN;
XX
WPI; 2002-599423/64.
XX
Novel isolated polypeptide (WOODEN LEG) with ability to regulate a set of
asymmetric cell divisions that establish vascular tissue in root and
hypocotyl development, useful for improving agronomically valuable
plants.
XX
Example 1; Page 151-157; 187pp; English.
XX
The invention relates to an isolated WOODEN LEG (WOL) polypeptide,
comprising 15 contiguous amino acids of a fully defined Arabidopsis
WOODEN LEG protein sequence of 1057 amino acids as given in the
specification, and to its encoding nucleic acid. The invention also
relates to an amino acid sequence of domains of protein, e.g., N-terminal
region, C-terminal domain, etc; or is a naturally occurring allelic
variant of the above mentioned polypeptide sequence. Expression levels of
the nucleic acid can be modified to improve the vasculature in transgenic
plants and enhance the agronomic properties of such plants. Also the WOL
promoter is used to drive expression of a heterologous coding sequence of
trees to improve wood production. The WOL nucleic acid may be used as a
molecular marker for a qualitative trait loci, e.g., longer roots or
enhanced wood production, in molecular breeding of crop plants. The
nucleic acid is also useful in DNA amplification assays to identify the
endogenous WOL genes, WOL mutant alleles and/or WOL expression products
in cultivars as compared to wild-type plants. They can also be used as
markers for linkage analysis of qualitative trait loci. The WOL protein
and/or antibodies can be used as diagnostic reagents in immunoassays to
detect expression of the WOL gene in cultivars and wild-type plants. The
WOL protein, its encoding nucleic acid, and its corresponding antibody
are useful for improving agronomically valuable plants e.g., trees. This
sequence represents a protein relating to the wooden leg (WOL) protein of
the invention

XX SQ Sequence 2150 AA;
Query Match 51.9%; Score 42; DB 5; Length 2150;
Best Local Similarity 53.8%; Pred. No. 1.5e+03;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GNSPRTQSPQNC 15
|||: |||
Db 345 GNSPRSCGNC 357

RESULT 37
AAR15781
ID AAR15781 standard; protein; 10 AA.
XX
AC AAR15781;
XX
DT 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 29-JAN-1992 (first entry)
XX
DE Farnesyl-protein transferase inhibitor (34).
XX
KW Farnesyl; transferase; FT; inhibitor; p21ras; rat.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 7.10
XX
PN WO9116340-A.
XX
PD 31-OCT-1991.
XX
PF 18-APR-1990; 90US-00510706.
XX
PR 18-APR-1990; 90US-00510706.
XX
PR 20-NOV-1990; 90US-00615715.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Brown MS, Goldstein JL, Reiss Y;
XX
WPI; 1991-339750/46.
XX
Compsn. comprising purified farnesyl-protein transferase - used to
inhibit attachment of farnesyl moiety to RAS protein in malignant cells
and to treat cancer.
XX
Claim 25; Page 68; 87pp; English.
XX
This peptide, the fragment indicated in the features, or the peptides
represented in AAR15751-81, AAR14723 and AAR14711 inhibit the rat FTs
represented in AAR14712-22. They show FT inhibition at an IC50 of 0.01-10
microM. The most potent inhibitors are ones in which phenylalanine occurs
at the third position of a tetrapeptide whose N-terminus is cysteine. The
inhibitors have a farnesyl acceptor or inhibitor sequence within its
structure and are capable of inhibiting the farnesylation of p21ras by
FT. See also AAR14711-23 and AAQ14541-47. (Updated on 09-JAN-2003 to add
missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 10 AA;
Query Match 50.6%; Score 41; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TQSPQNC 15
|||||
Db 1 TQSPQNC 7

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RESULT 38
AAR49742
ID AAR49742 standard; peptide; 10 AA.
XX AC AAR49742;
XX XX
XX XX 25-MAR-2003 (revised)
XX DT 08-AUG-1994. (first entry)
XX XX Farnesyltransferase-inhibitor.
XX DE
XX XX Farnesyltransferase-inhibitor; farnesyltransferase; FT; p21ras;
XX KW ras protein; farnesylation; cancer therapy.
XX XX Synthetic.
XX OS
XX XX WO9404561-A1.
XX FN
XX PD 03-MAR-1994.
XX XX
XX PF 24-AUG-1993; 93WO-US008062.
XX XX
XX PR 24-AUG-1992; 92US-00935087.
XX XX (TEXA ) UNIV TEXAS SYSTEM.
XX PA (GETH ) GENENTECH INC.
XX PI Brown MS, Goldstein JL, Reiss Y, Marsters JC;
XX XX WPI; 1994-083105/10.
XX DR
XX XX New farnesyltransferase inhibitors - used for inhibiting attachment of a
XX PT farnesyl moiety to a p19ras protein in malignant cells.
XX XX Disclosure; Page 33; 183pp; English.
XX CC
XX CC Peptides given in AAR49741-75, AAR49777-78 and AAR49785-88, which include
XX CC a family of tetrapeptides based on the recognition site (AAR49776) of
XX CC farnesyltransferase (FT), are potential anticancer agents that inhibit
XX CC FT, thereby preventing expression of p21ras. (Updated on 25-MAR-2003 to
XX CC correct PN field.)
XX XX Sequence 10 AA;
XX SQ
Query Match 50.6%; Score 41; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 TQSPQNC 15
Db |||||
1 TQSPQNC 7
RESULT 40
AAR04434
ID AAR04434 standard; peptide; 10 AA.
XX AC AAR04434;
XX XX
XX DT 30-JUL-1997 (first entry)
XX DE Farnesyl transferase peptide inhibitor used in cancer treatment.
XX KW Farnesyl transferase; inhibitor; cancer; tumour; neoplasia; prenyl;
XX KW ras protein; K-ras B; malignant; detection; identification.
XX OS Synthetic.
XX XX WO9634113-A2.
XX XX 31-OCT-1996.
XX PF 29-APR-1996; 96WO-US005969.
XX XX 27-APR-1995; 95US-00429964.
XX XX (TEXA ) UNIV TEXAS SYSTEM.
XX PA Brown MS, Goldstein JL, James GL;
XX PI WPI; 1996-497642/49.
XX DR
XX XX Assay for farnesyl transferase activity - by determining ability to
XX PT transfer farnesyl moiety to K-Ras B protein, partic. useful for
XX PT identifying inhibitors.
XX XX Disclosure; Page 33; 257pp; English.
XX PS
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RESULT 39
AAR77804
ID AAR77804 standard; protein; 10 AA.
XX AC AAR77804;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 23-JAN-1996 (first entry)
XX XX Farnesyl transferase inhibitor peptide, TQSPQNC5IM.
XX DE Farnesyl transferase; inhibitor; cancer; ras; p21.
XX KW Synthetic.
XX OS
XX XX US5420245-A.
XX FN
XX PD 30-MAY-1995.
XX XX
XX PF 03-APR-1992; 92US-00863169.
XX
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XX AA0433-W04465 are peptide inhibitors of farnesyl transferase (FT)
 CC activity. The peptides block the attachment of prenyl groups to ras
 CC proteins in malignant cells of patients suffering from cancer or a
 CC precancerous state and as such are used to treat cancer. The peptides
 CC were identified by determining the ability of candidate substances to
 CC inhibit a RT enzyme, by inhibiting the transfer of a farnesyl moiety to a
 CC K-RasB protein
 XX
 SQ Sequence 10 AA;
 Query Match 50.6%; Score 41; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 TQSPQC 15
 Db 1 TQSPQC 7
 RESULT 41
 AAU53546
 ID AAU53546 standard; protein; 68 AA.
 XX AC AAU53546;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #14442.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 FN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US012865.
 XX
 PR 21-APR-2000; 2000US-0199047P.
 PR 02-JUN-2000; 2000US-0208841P.
 PR 07-JUL-2000; 2000US-0216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR WPI; 2001-616774/71.
 DR N-PSDB; AAS59560.
 XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.
 XX
 PS Example 1; SEQ ID NO 14741; 1069pp; English.
 XX
 CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies

CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 68 AA;
 Query Match 50.6%; Score 41; DB 4; Length 68;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 SSPRTQSP 12
 Db 2 SSPRTQSP 9
 RESULT 42
 ABM50065
 ID ABM50065 standard; protein; 68 AA.
 XX AC ABM50065;
 XX
 DT 20-OCT-2003 (first entry)
 XX
 DE Propionibacterium acnes predicted ORF-encoded polypeptide #14741.
 XX
 KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine.
 XX
 OS Propionibacterium acnes.
 XX
 FN WO2003033515-A1.
 XX
 PD 24-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032727.
 XX
 PR 15-OCT-2001; 2001US-00978825.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vallie-Douglas J;
 XX
 DR WPI; 2003-381789/36.
 DR N-PSDB; ACF64489.
 XX
 PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX
 PS Example 1; SEQ ID NO 14741; 1481pp; English.
 XX
 CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising P. acnes polypeptides,
 CC via this method; a vaccine composition comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide; a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion

CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 68 AA;

Query Match 50.6%; Score 41; DB 6; Length 68;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SSPTQSP 12
 |||||
 Db 2 SSPTQSP 9

RESULT 43

ADL06330
 ID ADL06330 standard; protein; 539 AA.

XX AC ADL06330;

XX DT 06-MAY-2004 (first entry)

XX DE Amorpha fruticosa 4-coumaric acid:co-enzyme A ligase.

XX KW 4-coumaric acid:co-enzyme A ligase; CoA; 4CL; transgenic; plant; enzyme.

XX OS Amorpha fruticosa.

FH Key Location/Qualifiers

FT Misc-difference 465. .466

FT /note= "Encoded by GTTCCAATG"

XX FN CN1390940-A.

XX PD 15-JAN-2003.

XX PF 19-JUL-2002; 2002CN-00132631.

XX PR 19-JUL-2002; 2002CN-00132631.

XX PA (UYDA-) UNIV DALIAN SCI & ENG.

XX PI An L, Liu W, Su Q;

XX WPI; 2003-469215/45.

DR N-PSDB; ADL06329.

XX 4-coumaric acid: CoA ligase gene and its clone.

XX Disclosure; Page 7-8; 11pp; Chinese.

XX The present invention relates to the isolation of a plant 4-coumaric
 CC acid:Co-enzyme A (CoA) ligase (4CL) gene from Amorpha fruticosa, and the
 CC protein it encodes. Also disclosed is a clonal carrier pUC19/4CL
 CC containing 4CL, and an Escherichia coli cell JM109/pUC19/4CL containing
 CC the carrier. It can be used to configure genetically engineered bacteria
 CC for transgenic plants. The present sequence represents Amorpha fruticosa
 CC 4CL protein.

XX SQ Sequence 539 AA;

Query Match 50.6%; Score 41; DB 7; Length 539;
 Best Local Similarity 61.5%; Pred. No. 5e+02;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 3 GNSSPRTQSPNC 15
 ||||| :
 Db 374 GNSLPRNQSGEIC 386

RESULT 44

AAW26130

ID AAW26130 standard; protein; 542 AA.

XX AC AAW26130;

XX DT 17-OCT-2003 (revised)

XX DT 21-NOV-1997 (first entry)

XX DE 4-coumaric acid coenzyme A ligase.

XX KW 4-coumaric acid coenzyme A ligase; 4CL gene; tobacco; Nicotiana tabacum;
 lignin.

XX OS Nicotiana tabacum; L. SR1 strain.

XX PN JP09173069-A.

XX PD 08-JUL-1997.

XX PF 22-DEC-1995; 95JP-00334834.

XX PR 22-DEC-1995; 95JP-00334834.

XX PA (MITY) MITSUBISHI PAPER MILLS LTD.

XX DR WPI; 1997-397027/37.

XX DR N-PSDB; AAT80088.

XX 4-coumaric acid:coenzyme A ligase gene - used to reduce the lignin
 FT content of plants.

XX PS Claim 9; Page 6-8; 10pp; Japanese.

XX This sequence represents the 4-coumaric acid coenzyme A ligase (4CL) from
 CC Nicotiana tabacum strain SR1. The DNA encoding this sequence, or the 4CL
 CC gene fragments shown in AAT80086 and AAT80087, are introduced into a
 CC plant in the method of the invention. The method of the invention is for
 CC the reduction of lignin in a plant. The lignin content in a transformed
 CC plant can be reduced using this method. (Updated on 17-OCT-2003 to
 CC standardise OS field)

XX SQ Sequence 542 AA;

Query Match 50.6%; Score 41; DB 2; Length 542;

Best Local Similarity 61.5%; Pred. No. 5.1e+02;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GNSSPRTQSPNC 15

||||| :
 Db 377 GNSLPRNQSGEIC 389

RESULT 45

ADR86215

ID ADR86215 standard; protein; 747 AA.

XX AC ADR86215;

XX DT 04-NOV-2004 (first entry)

XX DE Aspergillus fumigatus essential gene protein #265.

XX KW Fungicide; Aspergillus fumigatus infection; Farmer's lung disease;
 drug screening.


```
OS Aspergillus fumigatus.
XX WO2004067709-A2.
XX 12-AUG-2004.
XX 16-JAN-2004; 2004WO-US001099.
XX 17-JAN-2003; 2003US-0441281P.
XX 13-JUN-2003; 2003US-0478196P.
XX (ELIT-) ELITRA PHARM INC.
XX (ELIT-) ELITRA CANADA LTD.
XX Jiang B, Hu W, Lemieux S, Roemer T;
XX WPI; 2004-594200/57.
XX N-PSDB; ADR85628.
XX New purified or isolated Aspergillus fumigatus nucleic acid molecule
XX encoding a gene product, useful for diagnosing and/or treating invasive
XX fungal infections, such as Farmer's lung disease.
XX Claim 1; SEQ ID NO 3265; 164pp; English.
XX The present invention relates to Aspergillus fumigatus genes that are
XX essential and are potential targets for drug screening. The methods and
XX compositions of the present invention are useful for diagnosing and/or
XX treating invasive Aspergillus fumigatus infection, including the allergic
XX forms of the disease, such as Farmer's lung disease. They can also be
XX used in various drug discovery purposes, such as expression of the
XX recombinant protein, hybridization assay and construction of nucleic acid
XX arrays. The present sequence represents an Aspergillus fumigatus
XX essential gene protein sequence, used during diagnosis and drug
XX development in the invention. These genes share a high degree of sequence
XX conservation with known essential genes of candida albicans. The sequence
XX data for this patent is not represented in the printed specification, but
XX was obtained in electronic format from WIPO.
XX Sequence 747 AA;
XX
XX Query Match 50.6%; Score 41; DB 8; Length 747;
XX Best Local Similarity 69.2%; Pred. No. 7.1e+02;
XX Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX Qy 1 LLGNSSPRTQSPQ 13
XX Db 204 LFTNSPPPEQSPQ 216
XX
XX RESULT 46
XX ADQ66060
XX ID ADQ66060 standard; protein; 791 AA.
XX AC ADQ66060;
XX 07-OCT-2004 (first entry)
XX Novel human protein sequence #1033.
XX osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
XX gene therapy; diagnostic marker; morbid state; osteoporosis;
XX neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
XX cancer.
XX Homo sapiens.
XX EP1440981-A2.
XX 28-JUL-2004.
XX 21-JAN-2004; 2004EP-00001196.
XX
XX Aspergillus fumigatus.
XX WO2004067709-A2.
XX 12-AUG-2004.
XX 16-JAN-2004; 2004WO-US001099.
XX 17-JAN-2003; 2003US-0441281P.
XX 13-JUN-2003; 2003US-0478196P.
XX (ELIT-) ELITRA PHARM INC.
XX (ELIT-) ELITRA CANADA LTD.
XX Jiang B, Hu W, Lemieux S, Roemer T;
XX WPI; 2004-594200/57.
XX N-PSDB; ADR85628.
XX New purified or isolated Aspergillus fumigatus nucleic acid molecule
XX encoding a gene product, useful for diagnosing and/or treating invasive
XX fungal infections, such as Farmer's lung disease.
XX Claim 1; SEQ ID NO 3265; 164pp; English.
XX The present invention relates to Aspergillus fumigatus genes that are
XX essential and are potential targets for drug screening. The methods and
XX compositions of the present invention are useful for diagnosing and/or
XX treating invasive Aspergillus fumigatus infection, including the allergic
XX forms of the disease, such as Farmer's lung disease. They can also be
XX used in various drug discovery purposes, such as expression of the
XX recombinant protein, hybridization assay and construction of nucleic acid
XX arrays. The present sequence represents an Aspergillus fumigatus
XX essential gene protein sequence, used during diagnosis and drug
XX development in the invention. These genes share a high degree of sequence
XX conservation with known essential genes of candida albicans. The sequence
XX data for this patent is not represented in the printed specification, but
XX was obtained in electronic format from WIPO.
XX Sequence 747 AA;
XX
XX Query Match 50.6%; Score 41; DB 8; Length 747;
XX Best Local Similarity 69.2%; Pred. No. 7.1e+02;
XX Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX Qy 1 LLGNSSPRTQSPQ 13
XX Db 204 LFTNSPPPEQSPQ 216
XX
XX RESULT 46
XX ADQ66060
XX ID ADQ66060 standard; protein; 791 AA.
XX AC ADQ66060;
XX 07-OCT-2004 (first entry)
XX Novel human protein sequence #1033.
XX osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
XX gene therapy; diagnostic marker; morbid state; osteoporosis;
XX neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
XX cancer.
XX Homo sapiens.
XX EP1440981-A2.
XX 28-JUL-2004.
XX 21-JAN-2004; 2004EP-00001196.
XX
XX 21-JAN-2003; 2003JP-00102206.
XX 09-MAY-2003; 2003JP-00131392.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
XX Yamamoto J, Isono Y, Nagai K, Irie R;
XX WPI; 2004-535376/52.
XX N-PSDB; ADQ63872.
XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
XX Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX Claim 1; SEQ ID NO 3221; 2449pp; English.
XX The invention relates to 2495 novel polynucleotides (I) and their encoded
XX polypeptides, sequences hybridizing to these nucleotides, sequences
XX encoding partial polypeptides and sequences having 70% or 90% identity to
XX the nucleotide and protein sequences. The nucleotides and polypeptides
XX are useful as diagnostic markers or therapeutic target for the diseases
XX or morbid states. They are also useful for treating osteoporosis,
XX neurological diseases, Alzheimer's diseases, Parkinson's diseases,
XX dementia and various cancers. This sequence corresponds to a protein
XX sequence of the invention.
XX Sequence 791 AA;
XX
XX Query Match 50.6%; Score 41; DB 8; Length 791;
XX Best Local Similarity 64.3%; Pred. No. 7.6e+02;
XX Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
XX Qy 1 LLGNSSPRTQSPQ 14
XX Db 29 LLGSKRPQSYQS 42
XX
XX RESULT 47
XX ADK52121
XX ID ADK52121 standard; protein; 871 AA.
XX AC ADK52121;
XX 20-MAY-2004 (first entry)
XX Human atopic dermatitis/psoriasis-associated protein #36.
XX Human atopic dermatitis; psoriasis; dermatological; anti-inflammatory;
XX antipsoriatic; rash.
XX Homo sapiens.
XX WO2004016785-A1.
XX 26-FEB-2004.
XX 06-AUG-2003; 2003WO-JP0099999.
XX 06-AUG-2002; 2002JP-00229319.
XX 14-MAY-2003; 2003JP-00136544.
XX (GENO-) GENOX RES INC.
XX (UKJU-) UNIV JUNTENDO.
XX Itoh M, Ogawa K, Shinagawa A, Sudo H, Ogawa H, Ra C;
XX Mitsuishi K;
XX WPI; 2004-214514/20.
XX N-PSDB; ADK52035.
XX Detecting atopic dermatitis or psoriasis comprises assaying levels of
XX expression of an indicator gene at a rash site and non-rash site of a
XX person with atopic dermatitis or psoriasis.
```

XX Example 2; SEQ ID NO 154; 484pp; Japanese.

XX The invention relates to detecting atopic dermatitis or psoriasis

XX comprising assaying the levels of expression of an indicator gene at a

XX rash site and non-rash site of a person with atopic dermatitis or

XX psoriasis, comparing these levels with those of a healthy person, and

XX determining that if the levels of indicators are higher or lower, then

XX this indicates the disease. Also included are a reagent for detecting

XX atopic dermatitis or psoriasis, a kit for screening for treatments, a

XX transgenic non human vertebrate animal models for the diseases, an agent

XX for inducing the diseases in mice and a DNA chip for assaying for the

XX indicator genes. The method is used for treatment, detection and animal

XX models for research of atopic dermatitis and psoriasis. The present

XX sequence is a protein encoded by an indicator gene of the invention.

XX SQ Sequence 871 AA;

Query Match 50.6%; Score 41; DB 8; Length 871;

Best Local Similarity 64.3%; Pred. No. 8.4e+02;

Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSPQN 14

Db 29 LLGRSKPRQSQS 42

|||||

|||||

RESULT 48

ADRO9093

ID ADR09093 standard; protein; 871 AA.

XX AC ADR09093;

XX DT 04-NOV-2004 (first entry)

XX DE Human protein useful for treating neurological disease Seq 2599.

XX KW human; oligo-capping method; diagnostic marker; gene therapy;

XX KW osteoporosis; neurological disease; Alzheimer's disease;

XX KW Parkinson's disease; dementia; short memory; cancer;

XX KW sense or motor function; emotional reaction; fear response; panic;

XX KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;

XX KW tranquiliser.

XX OS Homo sapiens.

XX PN EP1447413-A2.

XX PD 18-AUG-2004.

XX PF 12-FEB-2004; 2004EP-00003145.

XX PR 14-FEB-2003; 2003JP-00102207.

XX PR 09-MAY-2003; 2003JP-00131452.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;

XX Wakamatsu A, Ishii S, Nagai K, Irie R;

XX WPI; 2004-583265/57.

XX DR N-PSDB; ADR07137.

XX New 1995 cDNA, useful for treating osteoporosis, neurological diseases,

XX Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.

XX Claim 1; SEQ ID NO 2599; 2686pp; English.

XX This invention relates to novel, isolated full length human cDNA

XX molecules and the encoded proteins thereof. Specifically, it refers to

XX cDNA clones obtained by an oligo-capping method, where none of these

XX clones are identical to any known human mRNAs. The present invention

XX describes an immunoassay to identify agonists and antagonists, as well as

CC antibodies, antisense molecules and siRNAs that can all be used to bind

CC to and modulate expression of the cDNA molecules. As such, these

CC molecules are useful for diagnostic markers or therapeutic targets for

CC the various diseases or morbid states. In particular, they are useful in

CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's

CC disease, Parkinson's disease, dementia, short memory and various cancers,

CC as well as for maintaining equilibrium of sense or motor function, and

CC for treating emotional reaction, fear response and panic. Accordingly,

CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,

CC cyostatic and tranquiliser activities. This polypeptide is a protein

CC encoded by a full length human cDNA sequence of the invention. NOTE: This

CC sequence is not given in the sequence listing of the specification but

CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-

CC office.

XX SQ Sequence 871 AA;

Query Match 50.6%; Score 41; DB 8; Length 871;

Best Local Similarity 64.3%; Pred. No. 8.4e+02;

Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSPQN 14

Db 29 LLGRSKPRQSQS 42

|||||

|||||

RESULT 49

ABB58985

ID ABB58985 standard; protein; 1937 AA.

XX AC ABB58985;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 3747.

XX KW Drosophila; developmental biology; cell signalling; insecticide;

XX KW pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.

XX PR 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX DR N-PSDB; ABL03088.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

XX genes from Drosophila and for elucidating cell signaling and cell-cell

XX interactions.

XX Disclosure; SEQ ID NO 3747; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

XX capable of detecting 1000 or more genes from Drosophila. The invention is

XX useful in developmental biology and in elucidating cell signalling and

XX cell-cell interactions in higher eukaryotes for the development of

XX insecticides, therapeutics and pharmaceutical drugs. The invention

XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-

XX ABB72072). The sequence data for this patent did not form part of the

XX printed specification, but was obtained in electronic format directly

XX from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1937 AA;
Query Match 50.6%; Score 41; DB 4; Length 1937;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 3 GNSSPRTQSPQN 14
Db 1884 GQSSPAQQSPQD 1895
Query Match 49.4%; Score 40; DB 4; Length 71;
Best Local Similarity 57.1%; Pred. No. 83;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 1 LLGNSSPRTQSPQN 14
Db 29 LLTSGPQTTSPRN 42
Search completed: August 25, 2005, 11:41:00
Job time : 173 secs

XX SQ Sequence 1937 AA;
Query Match 50.6%; Score 41; DB 4; Length 1937;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 3 GNSSPRTQSPQN 14
Db 1884 GQSSPAQQSPQD 1895
RESULT 50
ABG20384
ID ABG20384 standard; protein; 71 AA.
XX AC ABG20384;
XX DT 13-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #20375.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI; 2001-639362/73.
XX DR N-PSDB; AAS84571.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX PS Claim 20; SEQ ID NO 50743; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (II) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have application in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 71 AA;

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OM protein - protein search, using sw model

Run on: August 25, 2005, 11:33:48 ; Search time 168 Seconds
(without alignments)
45.721 Million cell updates/sec

Title: US-10-803-541-2

Perfect score: 81

Sequence: 1 LLGNSSPRTQSPQNC 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	664	1	P02545 homo sapien
2	73	90.1	665	1	LAMA_HUMAN
3	69	85.2	135	2	P48679 rattus norv
4	69	85.2	665	1	Q8BNX5 mus musculu
5	69	85.2	665	1	P48678 mus musculu
6	69	85.2	665	2	Q91WF2 mus musculu
7	49	60.5	886	2	Q9DC21 mus musculu
8	48	59.3	172	2	Q6A050 mus musculu
9	48	59.3	852	2	Q6ZRC6 homo sapien
10	46	56.8	514	1	Q6CG31 yarrowia li
11	45	55.6	162	2	Q8VNR3 pseudomonas
12	44	54.3	180	2	Q9FTW9 oryza sativ
13	44	54.3	286	2	Q8BPZ3 mus musculu
14	44	54.3	443	2	Q96MH2 mus musculu
15	44	54.3	435	2	Q9VLQ0 homo sapien
16	44	54.3	643	2	Q91092 caenorhabdi
17	44	54.3	826	2	Q95Q79 caenorhabdi
18	44	54.3	970	1	Q8H852 oryza sativ
19	43	53.1	559	2	P53550 saccharomyc
20	43	53.1	2001	2	Q6C764 yarrowia li
21	42	51.9	161	2	Q8RZN9 oryza sativ
22	42	51.9	191	2	Q9DSW7 ascovirus d
23	42	51.9	291	2	Q38966 arabidopsis
24	42	51.9	690	1	Q7D016 agrobacteri
25	42	51.9	772	2	Q01603 drosophila
26	42	51.9	901	2	Q9LSE3 arabidopsis
27	42	51.9	962	1	Q6BY30 debaryomyce
28	42	51.9	2150	2	P59597 drosophila
29	42	51.9	4708	2	Q23863 dictyosteli
30	41	50.6	148	2	Q7TPH6 mus musculu
31	41	50.6	158	2	Q8Y147 anabaena sp
					Q7R2Z1 giardia lam

ALIGNMENTS

32	41	50.6	240	1	RCF2_PSEAE	O88638 pseudomonas
33	41	50.6	279	2	Q869Y4	Q869Y4 dictyosteli
34	41	50.6	439	2	Q8YUK2	Q8YUK2 anabaena sp
35	41	50.6	446	2	Q68CL1	Q68CL1 homo sapien
36	41	50.6	489	1	MURE_COXBU	Q83F28 coxiella bu
37	41	50.6	540	2	Q8W558	Q8W558 amorpha fru
38	41	50.6	542	1	4CL2_TOBAC	Q24146 nicotiana t
39	41	50.6	542	2	Q42943	Q42943 nicotiana t
40	41	50.6	556	2	Q6TUF8	Q6TUF8 rattus norv
41	41	50.6	577	2	Q8PIR2	Q8PIR2 xanthomonas
42	41	50.6	593	1	CDYL_MOUSE	Q9WTK2 mus musculu
43	41	50.6	599	2	Q64033	Q64033 mus sp. ant
44	41	50.6	871	2	Q96DR7	Q96DR7 homo sapien
45	41	50.6	871	2	Q6AZ96	Q6AZ96 homo sapien
46	41	50.6	871	2	Q6Q8Q8	Q6Q8Q8 homo sapien
47	41	50.6	1014	2	Q6DRCS	Q6DRCS brachydanio
48	41	50.6	2038	1	FSH_DROME	P13709 drosophila
49	41	50.6	2038	2	Q9W3L3	Q9W3L3 drosophila
50	40.5	50.0	470	1	SA12_XENLA	P40649 xenopus lae
51	40.5	50.0	567	2	Q6NUE6	Q6NUE6 xenopus lae
52	40	49.4	54	2	Q82RX5	Q82RX5 streptomyce
53	40	49.4	94	2	Q9PA03	Q9PA03 xylella fas
54	40	49.4	170	2	Q8N1L1	Q8N1L1 homo sapien
55	40	49.4	199	1	SOXE_SULAC	Q53765 sulfolobus
56	40	49.4	212	2	Q97WT6	Q97WT6 sulfolobus
57	40	49.4	257	1	HMMA_BRARE	Q03357 brachydanio
58	40	49.4	294	2	Q73708	Q73708 brachydanio
59	40	49.4	294	2	Q6PCA5	Q6PCA5 brachydanio
60	40	49.4	302	2	Q9VIT1	Q9VIT1 drosophila
61	40	49.4	311	2	Q8INV9	Q8INV9 drosophila
62	40	49.4	311	2	Q86NQ9	Q86NQ9 drosophila
63	40	49.4	318	2	Q8A804	Q8A804 bacteroides
64	40	49.4	345	2	Q8DH97	Q8DH97 synechococc
65	40	49.4	370	2	Q6CNE8	Q6CNE8 kluyveromycc
66	40	49.4	436	2	Q63DS5	Q63DS5 bacillus ce
67	40	49.4	452	2	Q8INW0	Q8INW0 drosophila
68	40	49.4	454	2	Q6LND8	Q6LND8 rat sp.
69	40	49.4	462	2	Q8IZ65	Q8IZ65 homo sapien
70	40	49.4	462	2	Q9H8Y6	Q9H8Y6 homo sapien
71	40	49.4	462	2	Q9HAJ1	Q9HAJ1 homo sapien
72	40	49.4	551	2	Q8UAQ1	Q8UAQ1 agrobacteri
73	40	49.4	622	2	Q9EQS1	Q9EQS1 cricetulus
74	40	49.4	641	2	Q6BY25	Q6BY25 debaryomyce
75	40	49.4	690	2	Q7Z6G6	Q7Z6G6 homo sapien
76	40	49.4	750	2	Q7Z6G6	Q7Z6G6 homo sapien
77	40	49.4	758	1	MEYE_PHOLL	Q7MZ74 photorhabd
78	40	49.4	758	2	Q9GQL5	Q9GQL5 trypanosoma
79	40	49.4	768	2	Q6IVB5	Q6IVB5 homo sapien
80	40	49.4	828	2	Q6FP48	Q6FP48 candida gla
81	40	49.4	870	2	Q9XTA4	Q9XTA4 bos taurus
82	40	49.4	934	2	Q6FY14	Q6FY14 candida gla
83	40	49.4	950	2	Q6AX98	Q6AX98 xenopus lae
84	40	49.4	950	2	Q9Y5K9	Q9Y5K9 homo sapien
85	40	49.4	962	2	Q80UZ8	Q80UZ8 mus musculu
86	40	49.4	962	2	Q91YY9	Q91YY9 mus musculu
87	40	49.4	1004	2	Q6S8V6	Q6S8V6 homo sapien
88	40	49.4	1008	2	Q8AY57	Q8AY57 fundulus he
89	40	49.4	1012	1	IF2C_PHAVU	P57997 phaseolus v
90	40	49.4	1017	1	AI42_CHICK	P24797 gallus gall
91	40	49.4	1017	2	Q90X34	Q90X34 brachydanio
92	40	49.4	1017	2	Q9DGL5	Q9DGL5 brachydanio
93	40	49.4	1020	1	AI42_HUMAN	P50993 homo sapien
94	40	49.4	1020	1	AI42_RAT	P06686 rattus norv
95	40	49.4	1020	2	Q6PIE5	Q6PIE5 mus musculu
96	40	49.4	1022	2	Q6PAG0	Q6PAG0 xenopus lae
97	40	49.4	1022	2	Q6ZQ49	Q6ZQ49 mus musculu
98	40	49.4	1025	2	Q91WH7	Q91WH7 mus musculu
99	40	49.4	1030	1	ATHA_XENLA	Q92126 xenopus lae
100	40	49.4	1032	1	ATHA_MOUSE	Q64436 mus musculu

RP	Am. J. Hum. Genet. 71:426-431(2002).	DT	05-JUL-2004 (Rel. 44, Last annotation update)
RP	[15]	DB	Lamin A.
RP	VARIANT WADA HIS-527.	GN	Name=Lma; Synonyms=Lmn1;
RP	PubMed=12075506.	OS	Rattus norvegicus (Rat).
RA	Novelli G., Muchir A., Sangiulio F., Helbling-Leclerc A.,	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RA	D'Apice M.R., Massart C., Capon P., Sbraccia P., Federici M.,	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RA	Lauro R., Tufisco C., Pallotta R., Scarano G., Dallapiccola B.,	OX	NCBI_TaxID=10116;
RA	Merlini L., Bonne G.	RN	[1]
RT	"Mandibuloacral dysplasia is caused by a mutation in LMNA-encoding	RP	SEQUENCE FROM N.A.
RT	lamin A/C."	RP	MEDLINE=93050186; PubMed=1426247; DOI=10.1016/0014-5793(92)80927-9;
RL	Am. J. Hum. Genet. 71:426-431(2002).	RA	Ozaki T., Sakiyama S.;
RL	[16]	RT	"Lamin A gene expression is specifically suppressed in v-src-
RP	VARIANT CMD1A ASSOCIATED WITH QUADRICEPS MYOPATHY HIS-377.	RL	transformed cells."
RP	MEDLINE=22560388; PubMed=12673789; DOI=10.1002/humu.10170;	RN	[2]
RA	Charniot J.-C., Pascal C., Bouchier C., Sebillion P., Salama J.,	RP	SPRAIN-Sprague-Dawley; TISSUE=Liver;
RA	Duboscq-Bidot L., Peuchmaud M., Deenos M., Artigou J.-Y., Komajda M.;	RC	Jonnalagadda V.S., Farnak V.K.;
RT	"Functional consequences of an LMNA mutation associated with a new	RA	Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RT	cardiac and non-cardiac phenotype."	CC	-1- FUNCTION: Lamins are components of the nuclear lamina, a fibrous
RL	Hum. Mutat. 21:473-481(2003).	CC	layer on the nucleoplasmic side of the inner nuclear membrane,
RN	[17]	CC	which is thought to provide a framework for the nuclear envelope
RP	VARIANT LHCP LEU-133.	CC	and may also interact with chromatin.
RP	MEDLINE=22515017; PubMed=12629077; DOI=10.1210/jc.2002-021506;	CC	-1- SUBCELLULAR LOCATION: Nuclear.
RA	Caux F., Duboclard E., Lascos O., Buendia B., Chazouilleres O.,	CC	-1- ALTERNATIVE PRODUCTS:
RA	Cohen A., Courvalin J.-C., Laroche L., Capeau J., Vigouroux C.,	CC	Event=Alternative splicing; Named isoforms=2;
RA	Christin-Maitre S.;	CC	Comment=Isoform A and isoform C are present in equal amounts in
RT	"A new clinical condition linked to a novel mutation in lamins A and C	CC	the lamina of mammals;
RT	with generalized lipodystrophy, insulin-resistant diabetes, disseminated	CC	Name=Lamin A;
RT	leukodermic papules, liver steatosis and cardiomyopathy."	CC	Isoid=P48679-1; Sequence=Displayed;
RL	J. Clin. Endocrinol. Metab. 88:1006-1013(2003).	CC	Name=Lamin C;
RN	[18]	CC	Isoid=P48679-2; Sequence=Not described;
RP	VARIANTS HGPS CYS-471; CYS-527 AND SER-608.	CC	-1- PFM: Increased phosphorylation of the lamins occurs before
RP	PubMed=12768443; DOI=10.1007/s10038-003-0025-3;	CC	envelope disintegration and probably plays a role in regulating
RA	Cao H., Hegele R.A.;	CC	lamin associations.
RT	"LMNA is mutated in Hutchinson-Gilford progeria (MIM 176670) but not	CC	-1- MISCELLANEOUS: The structural integrity of the lamina is strictly
RT	in Wiedemann-Rautenstrauch progeroid syndrome (MIM 264090)."	CC	controlled by the cell cycle, as seen by the disintegration and
RL	J. Hum. Genet. 48:271-274(2003).	CC	formation of the nuclear envelope in prophase and telophase,
RN	[19]	CC	respectively.
RP	VARIANT ATFB LYS-161.	CC	-1- SIMILARITY: Belongs to the intermediate filament family.
RP	PubMed=12920062;	CC	-1- CAUTION: Ref.1 sequence differs from that shown in the N- and C-
RA	Sebillion P., Bouchier C., Bidot L.D., Bonne G., Ahamed K., Charron P.,	CC	terminal due to frameshifts.
RA	Drouin-Garraud V., Millaire A., Desrumeaux G., Benachic A.,	CC	-----
RA	Charniot J.-C., Schwartz K., Villard E., Komajda M.;	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
RT	"Expanding the phenotype of LMNA mutations in dilated cardiomyopathy	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
RT	and functional consequences of these mutations."	CC	the European Bioinformatics Institute. There are no restrictions on its
RL	J. Med. Genet. 40:560-567(2003).	CC	use by non-profit institutions as long as its content is in no way
RN	[20]	CC	modified and this statement is not removed. Usage by and for commercial
RP	VARIANTS WERNER SYNDROME PRO-57 AND ARG-140.	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
RP	PubMed=12927431; DOI=10.1016/S0140-6736(03)14069-X;	CC	or send an email to license@sib-sib.ch).
RA	Chen L., Lee L., Kudlow B.A., Dos Santos H.G., Sletvold O.,	CC	-----
RA	Shafeghati Y., Botha E.G., Garg A., Hanson N.B., Martin G.M.,	CC	EMBL; X66870; CAA47342.1; ALT_FRAME.
RA	Mian I.S., Kennedy B.K., Oshima J.;	CC	EMBL; X76297; P02545; 11FR.
RT	"LMNA mutations in atypical Werner's syndrome."	CC	RGD; 620456; Lmna.
RL	Lancet 362:440-445(2003).	CC	InterPro; IPR001664; IF.
RN	[21]	CC	InterPro; IPR001322; IF tail_C.
RP	VARIANTS HGPS LYS-145 AND SER-608.	CC	Pfam; PF00038; Filament; 1.
RP	PubMed=12714972; DOI=10.1038/nature01629;	CC	Pfam; PF00932; IF_tail; 1.
RA	Eriksson M., Brown W.T., Gordon L.B., Glynn M.W., Singer J., Scott L.,	CC	PROSITE; PS00226; IF; 1.
RA	Erdo M.R., Robbins C.M., Moses T.Y., Berglund P., Dutra A., Pak E.,	CC	Alternative splicing; Coiled coil; Intermediate filament; Lipoprotein;
RT	Query Match 100.0%; Score 81; DB 1; Length 664;	CC	Alternative splicing; Coiled coil; Intermediate filament; Lipoprotein;
RT	Best Local Similarity 100.0%; Pred. No. 0.00014;	CC	Nuclear protein; Phosphorylation; Prenylation.
RT	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	-----
OY	1 LLGNSSPRTQSPNC 15	FT	DOMAIN 1 33 Head.
Db	647 LLGNSSPRTQSPNC 661	FT	DOMAIN 34 383 Rod.
RESULT 2		FT	DOMAIN 384 665 Tail.
LAMA RAT		FT	DOMAIN 34 70 Coil 1A.
AC P48679;		FT	DOMAIN 71 80 Linker 1.
DT 01-FEB-1996 (Rel. 33, Created)		FT	DOMAIN 81 218 Coil 1B.
DT 01-FEB-1996 (Rel. 33, Last sequence update)		FT	DOMAIN 219 242 Linker 2.
		FT	DOMAIN 243 383 Coil 2.
		FT	SITE 325 325 Stutter (By similarity).
		FT	DOMAIN 417 422 Nuclear localization signal (Potential).
		FT	LIPID 662 S-farnesyl cysteine (By similarity).

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FT CONFLICT 470 470 K -> R (in Ref. 1).
FT CONFLICT 524 524 T -> S (in Ref. 1).
FT CONFLICT 584 584 R -> P (in Ref. 1).
FT CONFLICT 606 606 A -> P (in Ref. 1).
SQ SEQUENCE 665 AA; 74323 MW; 9CC553005C8534B4 CRC64;

Query Match 90.1%; Score 73; DB 1; Length 665;
Best Local Similarity 93.3%; Pred. No. 0.0029;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LLGNSPRTQSPQNC 15
Db 648 LLGNSPRTQSPQNC 662

RESULT 3
Q8BNX5 PRELIMINARY; PRT; 135 AA.
AC Q8BNX5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult male aorta and vein cDNA, RIKEN full-length
DE enriched library, clone: A530030G15 product: lamin A, full insert
DE sequence. (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
```

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RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tegawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK079972; BAC37795.1; -.
DR HSSP; P02545; IIVT. -.
FT NON TER 1
SQ SEQUENCE 135 AA; 13855 MW; AAEB58E54D9242B0 CRC64;

Query Match 85.2%; Score 69; DB 2; Length 135;
Best Local Similarity 86.7%; Pred. No. 0.0022;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LLGNSPRTQSPQNC 15
Db 118 LLGNSPRTQSPQNC 132

RESULT 4
LAMA_MOUSE
ID LAMA_MOUSE STANDARD; PRT; 665 AA.
AC P48678; P97859;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lamin A.
GN Name=Lama; Synonym=Lmnl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95300954; PubMed=7781761; DOI=10.1016/0014-5793(95)00453-G;
RA Nakajima N., Abe K.;
RT "Genomic structure of the mouse A-type lamin gene locus encoding
RT somatic and germ cell-specific lamins.";
RL FEBS Lett. 365:108-114(1995).
RN [2]
RP SEQUENCE OF 1-568 FROM N.A.
RX MEDLINE=89247440; PubMed=2719959; DOI=10.1016/0167-4781(89)90179-6;
RA Riedel W., Werner D.;
RT "Nucleotide sequence of the full-length mouse lamin C cDNA and its
RT deduced amino-acid sequence.";
RL Biochim. Biophys. Acta 1008:119-122(1989).
RN [3]
RP SEQUENCE OF 235-665 FROM N.A.
RX MEDLINE=93144345; PubMed=7916626; DOI=10.1016/0167-4781(93)90072-L;
RA Nakajima N., Sado T.;
RT "Nucleotide sequence of a mouse lamin A cDNA and its deduced amino
RT acid sequence.";
RL Biochim. Biophys. Acta 1171:311-314(1993).
CC -!- FUNCTION: Lamins are components of the nuclear lamina, a fibrous
CC layer on the nucleoplasmic side of the inner nuclear membrane,
CC which is thought to provide a framework for the nuclear envelope
CC and may also interact with chromatin.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Isoform A and isoform C are present in equal amounts in
CC the lamina of mammals;
```


CC Name=A;
CC IsoId=P48678-1; Sequence=Displayed;
CC Name=B;
CC IsoId=P11516-1; Sequence=External;
CC Name=C;
CC IsoId=P11516-2; Sequence=External;
CC -!- PTM: Increased phosphorylation of the lamins occurs before
CC envelope disintegration and probably plays a role in regulating
CC lamin associations.
CC -!- MISCELLANEOUS: The structural integrity of the lamina is strictly
CC controlled by the cell cycle, as seen by the disintegration and
CC formation of the nuclear envelope in prophase and telophase,
CC respectively.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -!- CAUTION: Ref.1 sequence differs from that shown from position 582
CC onward and is longer (702 AA) due to a frameshift.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D49733; BAA08569.1; -.
CC EMBL; D49732; BAA08569.1; JOINED.
CC EMBL; D49734; BAA08569.1; JOINED.
CC EMBL; D49735; BAA08569.1; JOINED.
CC EMBL; D13181; BAA02476.1; -.
CC HSSP; P02545; 1IFR.
CC MGD; MGI:96794; Lmna.
CC GO; GO:0005638; C:lamin filament; IDA.
CC GO; GO:0005634; C:nucleus; IDA.
CC GO; GO:0005515; F:protein binding; IPI.
CC InterPro; IPR001664; IF.
CC InterPro; IPR001322; IF_tail_C.
CC Pfam; PF00038; Filament_1.
CC Pfam; PF00932; IF_tail; 1.
CC PROSITE; PS00226; IF; 1.
CC Alternative splicing; Coiled coil; Intermediate filament; Lipoprotein;
CC Nuclear protein; Phosphorylation.
CC DOMAIN 1 33 Head.
CC DOMAIN 34 383 Tail.
CC DOMAIN 384 665 Coiled coil 1A.
CC DOMAIN 34 70 Linker 1.
CC DOMAIN 71 80 Coiled coil 1B.
CC DOMAIN 81 218 Linker 2.
CC DOMAIN 219 242 Coiled coil 2.
CC DOMAIN 243 383 Scutter (By similarity).
CC SITE 325 325 Nuclear localization signal (Potential).
CC DOMAIN 417 422 Nuclear localization signal (By similarity).
CC LIPID 662 662 S-farnesyl cysteine (By similarity).
CC CONFLICT 118 119 AR -> VC (in Ref. 2).
CC CONFLICT 401 401 R -> P (in Ref. 2).
CC CONFLICT 439 440 RV -> WL (in Ref. 2).
CC CONFLICT 623 623 A -> V (in Ref. 1).
CC SEQUENCE 665 AA; 74209 MW; 5434B6D60A04CB15 CRC64;

Query Match 85.2%; Score 69; DB 1; Length 665;
Best Local Similarity 86.7%; Pred. No. 0.013;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLGNSSPRTPSQPNC 15
Db 648 LLGNSSPRSQSQNC 662
|||||:|||||

RESULT 5
Q91WF2 PRELIMINARY; PRT; 665 AA.
AC Q91WF2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lamin A, isoform A.
GN Name=Lmna;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,
RA Diatchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC EMBL; BC015302; AAH15302.1; -.
CC PIR; S28182; S28182.
CC HSSP; P02545; 1IFR.
CC MGD; MGI:96794; Lmna.
CC GO; GO:0005638; C:lamin filament; IDA.
CC GO; GO:0005634; C:nucleus; IDA.
CC GO; GO:0005515; F:protein binding; IPI.
CC Pfam; PF00038; Filament_1.
CC Pfam; PF00932; IF_tail; 1.
CC PROSITE; PS00226; IF; 1.
CC Intermediate filament.
CC SEQUENCE 665 AA; 74237 MW; 5434F574803FCB15 CRC64;

Query Match 85.2%; Score 69; DB 2; Length 665;
Best Local Similarity 86.7%; Pred. No. 0.013;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLGNSSPRTPSQPNC 15
Db 648 LLGNSSPRSQSQNC 662
|||||:|||||

RESULT 6
Q9DC21 PRELIMINARY; PRT; 665 AA.
AC Q9DC21;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
DE clone:120006N04 product:lamin A, full insert sequence.
GN Name=Lmna;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RX "High-efficiency full-length cDNA cloning.";
 RT Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RX "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX The FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RX Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RA "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RA "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multipipillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the intermediate filament family.
 DR EMBL; AK004619; BAB33415.1; -;
 DR PIR; S28182; S28182.
 DR HSSP; P02545; 1IFR.
 DR MGD; MGI:96794; Lmna.
 DR GO; GO:0005638; C:lamins; IDA.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR InterPro; IPR011000; ApoLp_III_like.
 DR InterPro; IPR001664; IF.
 DR InterPro; IPR001322; IF tail_C.
 DR Pfam; PF00038; Filament7_1.

DR Pfam; PF00932; IF tail_1.
 DR PROSITE; PS00226; IF; 1.
 RW Intermediate filament.
 SQ SEQUENCE 665 AA; 74299 MW; B69098CFE028C078 CRC64;
 Query Match 85.2%; Score 69; DB 2; Length 665;
 Best Local Similarity 86.7%; Pred. No. 0.013;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LLGNSSPRTQSPQC 15
 Db 648 LLGNSSPRTQSPQC 662
 RESULT 7
 Q6A050 PRELIMINARY; PRT; 886 AA.
 AC Q6A050;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE MKIAA0545 protein (fragment).
 GN Name=MKIAA0545;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryonic tail;
 RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
 RA Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
 RA Nagase T., Ohara O., Koga H.;
 RA "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
 RT IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous
 RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
 RT Randomly Sampled from Size-Fractionated Libraries.";
 RL DNA Res. 11:205-218(2004).
 CC -1- SIMILARITY: Contains 1 PDZ/DHR domain.
 DR EMBL; AK172968; BAD32246.1; -;
 DR GO; GO:0005515; F:protein binding; IEA.
 DR InterPro; IPR001478; PDZ.
 DR InterPro; IPR011036; PH-related.
 DR Pfam; PF00595; PDZ; 1.
 DR SMART; SM00228; PDZ; 1.
 DR PROSITE; PSS0106; PDZ; 1.
 FT NON TER 1
 SQ SEQUENCE 886 AA; 97239 MW; F14C04074685734E CRC64;
 Query Match 60.5%; Score 49; DB 2; Length 886;
 Best Local Similarity 75.0%; Pred. No. 33;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LGNSSPRTQSPQ 13
 Db 629 LGSHSPKTQSPQ 640
 RESULT 8
 Q6ZRC6 PRELIMINARY; PRT; 172 AA.
 AC Q6ZRC6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein FLJ46471.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;

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RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Nakahori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA Maguchi Y., Nagai K., Isegai T.,
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK128329; BAC7386.1; -.
SQ SEQUENCE 172 AA; 19030 MW; 93988457BC63AC2E CRC64;

Query Match 59.3%; Score 48; DB 2; Length 172;
Best Local Similarity 76.9%; Pred. No. 7.8;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 LLGNSPRTQSPQ 13
Db 108 VLGYSPPRTLSFQ 120

RESULT 9
Q6CG31 PRELIMINARY; PRT; 852 AA.
ID Q6CG31
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similarity.
GN ORFNames=YALI0B01320g;
OS Yarrowia lipolytica CLIB99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talia E.,
RA Goffard N., Franchin S., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissane A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.P., Straub M.L., Suleau A.,
RA Swennene D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Winkler P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382128; CAG82598.1; -.
DR InterPro; IPR008941; TPR-like.
SQ SEQUENCE 852 AA; 96983 MW; 178484411DE6302B CRC64;

Query Match 59.3%; Score 48; DB 2; Length 852;
Best Local Similarity 57.1%; Pred. No. 46;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 2 LGNSPRTQSPQNC 15
Db 313 VGNLSPGQBDPQNC 326

RESULT 10

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HUTH_PSEFL STANDARD; PRT; 514 AA.
ID Q6WMR3;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Histidine ammonia-lyase (EC 4.3.1.3) (Histidase).
GN Name=huth; Synonyms=huth-1;
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SBW25;
RA Zhang X.X.;
RT "Using RIVET to study histidine availability in planta for plant
RT growth-promoting Pseudomonas fluorescens SBW25";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: L-histidine = urocanate + NH(3).
CC -|- PATHWAY: Histidine degradation; first step.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC -|- PTM: Contains an active site 4-methylidene-imidazole-5-one (MIO),
CC which is formed autocatalytically by cyclization and dehydration
CC of residues Ala-Ser-Gly (By similarity).
CC -|- SIMILARITY: Belongs to the PAL / histidase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
DR EMBL; AJ421809; CAD19072.1; -.
DR HSSP; P21310; 1GKM.
DR HAMAP; MF 00229; -.
DR InterPro; IPR005921; Huth.
DR InterPro; IPR008948; L-Aspartase-like.
DR InterPro; IPR001106; Phe/His_NH3lyase.
DR Pfam; PF00221; PAL; 1.
DR TIGRFAMs; TIGR01225; huth; 1.
DR PROSITE; PS00488; PAL_HISTIDASE; 1.
DR Histidine metabolism; Lyase.
KW CROSSLINK 143 145 5-Imidazolinone (Ala-Gly) (By
FT MOD_RES 144 144 similarity).
FT 2,3-didehydroalanine (Ser) (By
FT similarity).
FT SEQUENCE 514 AA; 54478 MW; E89C067DA6985492 CRC64;

Query Match 56.8%; Score 46; DB 1; Length 514;
Best Local Similarity 66.7%; Pred. No. 55;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 1 LLGNSPRTQSPQNC 15
Db 260 LLGESSQVSHQNC 274

RESULT 11
Q9FWN9 PRELIMINARY; PRT; 162 AA.
ID Q9FWN9 QTXCD4;
AC Q9FWN9; QTXCD4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative lipid transfer protein.
GN ORFNames=OSJNBa0015J15.17;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.

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RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto K., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuna N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kinata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Yoshishino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Nishikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shinizu F., Wabebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45 (2004).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshylyuk S., Carninci P., Prange C.,
RA Rask S.S., Loquellano N.J., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish U., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Petrozello J., Carter P.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK056946; BAB71319.1; -;
DR EMBL; BC025970; AAH25970.1; -;
DR EMBL; AY598322; AAT06733.1; -;
SQ SEQUENCE 286 AA; 32418 MW; 58576D72096A9A6F CRC64;

Query Match 54.3%; Score 44; DB 2; Length 286;
Best Local Similarity 80.0%; Pred. No. 61;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 SPRTQSPQNC 15
|||||||

Db 71 SPRTQSPQNC 80
RESULT 14
Q9VLQ0 PRELIMINARY; PRT; 443 AA.
ID Q9VLQ0;
AC Q9VLQ0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CG7851-PA (RH11377P).
GN Drosophila melanogaster (Fruit fly).
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Fodor C., Gabrielian A.E., Garg N.P., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hootin K., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.S., Kodra C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laake P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodger, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu S.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RP SEQUENCE FROM N.A.


```

RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U80443; AAK68201.1; -.
DR HSSP; P11171; 1G33.
DR WormBase; WBGene0001491; fgm-4.
DR WormPep; C2A11.8b; CE27724.
DR CO; GO:0005856; C:cytoskeleton; IEA.
DR InterPro; IPR000299; Band 4.1.1.
DR InterPro; IPR009065; FERM.
DR InterPro; IPR011036; PH related.
DR Pfam; PF00373; Band 41; 1.
DR PRINTS; PR00935; BANO41.
DR SMART; SM00295; B41; 1.
DR PROSITE; PS50057; FERM_3; 1.
SQ SEQUENCE 643 AA; 72668 MW; F7C1058404EA7182 CRC64;

Query Match 54.3%; Score 44; DB 2; Length 643;
Best Local Similarity 61.5%; Pred. No. 1.5e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLGNSPRTQSPQ 13
Db 40 IIGNEFPRTQSAQ 52

RESULT 17
QH852 PRELIMINARY; PRT; 826 AA.
AC QH852;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative Nonclathrin coat protein gamma-like protein.
GN Name=OJ1626B05.5;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Saski C.,
RA Currie J., Collura K.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AC104473; AAN60990.1; -.
DR HSSP; Q9Y678; 1R4X.
DR Gramene; Q9H852; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002553; Adaptin_N.
DR InterPro; IPR008938; ARM.
DR Pfam; PF01602; Adaptin_N; 1.
SQ SEQUENCE 826 AA; 91994 MW; 2E44E7BB3BA8B61E CRC64;

Query Match 54.3%; Score 44; DB 2; Length 826;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LLGNSPRTQSP 12
Db 403 LLGNEGRTSDP 414

RESULT 18
PSU1_YEAST STANDARD; PRT; 970 AA.
AC P53550;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE mRNA decapping protein 2 (PSU1 protein).
GN Name=DCP2; Synonyms=PSU1; OrderedLocusNames=YNL118C; ORFNames=N1917;
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D273-10B;
RA Tzagoloff A.A.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97245296; PubMed=9090055;
RX DOI=10.1002/(SICI)1097-0061(19970315)13:3<261::AID-YEA64>3.0.CO;2-L;
RA de Antoni A., D'Angelo M., Dal Pero F., Sartorello F., Pandolfo D.,
RA Pallavicini A., Ianfranchi G., Valle G.;
RT "The DNA sequence of cosmid 14-13b from chromosome XIV of
RT Saccharomyces cerevisiae reveals an unusually high number of
RT overlapping open reading frames.";
RL Yeast 13:261-266(1997).
RN [3]
RP INTERACTION WITH DCP1.
RX MEDLINE=99438017; PubMed=10508173; DOI=10.1093/emboj/18.19.5411;
RA Duncley T., Parker R.;
RT "The DCP2 protein is required for mRNA decapping in Saccharomyces
RT cerevisiae and contains a functional MutT motif.";
RL EMBO J. 18:5411-5422(1999).
CC -!- FUNCTION: Required for the production of active decapping enzyme,
CC perhaps in a process requiring the hydrolysis of a pyrophosphate
CC bond. Decapping is the major pathway of mRNA degradation in yeast.
CC It occurs through deadenylation, decapping and subsequent 5' to 3',
CC exonucleolytic decay of the transcript body.
CC -!- SUBUNIT: Interacts with DCP1.
CC -!- SIMILARITY: Belongs to the Nudix hydrolase family.
CC -----
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CC -----
CC EMBL; L43065; AAA68866.1; -.
CC EMBL; Z69382; CAA93389.1; -.
CC EMBL; Z71394; CAA95998.1; -.
CC PIR; S63059; S63059.
CC GerMOnline; 143124; -.
CC SGD; S00005062; DCP2.
CC GO; GO:0000932; C:cytoplasmic mRNA processing body; IEA.
CC GO; GO:0005634; C:nucleus; IEA.
CC GO; GO:0008047; F:enzyme activator activity; IEA.
CC GO; GO:0016787; F:hydrolase activity; IEA.
CC GO; GO:0003729; F:mRNA binding; IPI.
CC GO; GO:0000290; P:deadenylation-dependent decapping; IEA.
CC InterPro; IPR007722; DCP2.
CC InterPro; IPR000086; NUDIX_hydrolase.
CC Pfam; PF05026; DCP2; 1.
CC Pfam; PF00293; NUDIX; 1.
CC PRINTS; PR00502; NUDIXFAMILY.
CC PROSITE; PS00893; NUDIX; 1.
KW Hydrolase.
FT DOMAIN 134 155 Nudix box.
FT DOMAIN 436 439 Poly-Ser.
FT CONFLICT 425 425 P -> L (in Ref. 1).
SQ SEQUENCE 970 AA; 108667 MW; D53CA2C5A546FA4A CRC64;
```



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Query Match          54.3%; Score 44; DB 1; Length 970;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GNSSPRTQSPON 14
Db 595 GKSPSTQSKQN 606

RESULT 19
ID Q6C764 PRELIMINARY; PRT; 559 AA.
AC Q6C764;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Similar to sp|P38140 Saccharomyces cerevisiae YBR239c.
GN ORFNames=YAL10E03410g;
OS Yarrowia lipolytica CLIB99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisarane A., Boyer J., Cattolico L., Confanioli P., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Niclaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swemene D., Tekaia F., Wesolowski-louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Winkler P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Contains 1 Zn(2)-Cys(6) fungal-type binuclear cluster
CC domain.
DR EMBL; CR382131; CAG79077.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001138; Fungi_Trcsrp_N.
DR Pfam; PF00172; Zn_c1us; 1.
DR SMART; SM00066; GAL4; 1.
DR PROSITE; PS00048; ZN2_CV6_FUNGAL_2; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Transcription;
KW Transcription regulation; Zinc.
SQ SEQUENCE 559 AA; 61447 MW; DA57240C9E634D0B CRC64;

Query Match          53.1%; Score 43; DB 2; Length 559;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Qy 1 LLGNS--SPRTQSPON 14
Db 235 LLGNSQSPNTHSPHN 250

RESULT 21
ID Q9DSW7 PRELIMINARY; PRT; 161 AA.
AC Q9DSW7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE Hypothetical protein.
OS Ascovirus DpAV4.
OC Viruses; dsDNA viruses, no RNA stage; Ascoviridae; Ascovirus.
OX NCBI_TaxID=113365;
RN [1]

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RESULT 20

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Q8RZN9 PRELIMINARY; PRT; 2001 AA.
ID Q8RZN9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative polyprotein.
GN Name=B1065E10.26;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakaishima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yanagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
RN EMBL; AP003561; BAB90375.1; -.
DR Gramene; Q8RZN9; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR005162; Retrotrans_gag.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR001584; Rve.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF03732; Retrotrans_gag; 1.
DR Pfam; PF00075; RNaseH; 1.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF00078; RVT_1; 1.
KW Polyprotein; RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 2001 AA; 225569 MW; 93EEF5FE01BBFD7 CRC64;

Query Match          53.1%; Score 43; DB 2; Length 2001;
Best Local Similarity 57.1%; Pred. No. 7.7e+02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSPRTQSPON 14
Db 231 ILQSNIPRTQPQN 244

RESULT 21
ID Q9DSW7 PRELIMINARY; PRT; 161 AA.
AC Q9DSW7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE Hypothetical protein.
OS Ascovirus DpAV4.
OC Viruses; dsDNA viruses, no RNA stage; Ascoviridae; Ascovirus.
OX NCBI_TaxID=113365;
RN [1]

```


RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milghina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of *Drosophila melanogaster*.";
RA Science 287:2185-2195(2000).
[4]
RN GENOME REANNOTATION.
RX MEDLINE=22426069; PubMed=12537572;
RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettecous B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
[5]
RN GENOME REANNOTATION.
RX PubMed=14709175; DOI=10.1186/gb-2003-5-1-r3;
RA Hild M., Beckmann B., Haas S.A., Koch B., Solovyyev V., Busold C.,
RA Fellenberg K., Boutsos M., Vingron M., Sauer F., Hoheisel J.D.,
RA Paro R.;
RT "An integrated gene annotation and transcriptional profiling approach
RT towards the full gene content of the *Drosophila* genome.";
RL Genome Biol. 5:RESEARCH0003.1-RESEARCH0003.17(2003).
CC -!- CATALYTIC ACTIVITY: Donor + H(2)O(2) = oxidized donor + 2 H(2)O.
CC -!- COPACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per
CC subunit [by similarity].
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: Belongs to the peroxidase family. XPO subfamily.

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DR EMBL; X68131; CAA48238.1; -;
DR EMBL; AY541497; AAS48542.1; -;
DR EMBL; AE003715; AAS65161.1; -;
DR EMBL; BK002598; DAA04104.1; ALT_INIT.
DR PIR; S28222; S28222.
DR HSSP; P05164; 1D5L.
DR FlyBase; FBgn0004577; Pxd.
DR InterPro; IPR002007; Anim_peroxidase.
DR InterPro; IPR002016; Peroxidase.
DR InterPro; IPR010255; Peroxidase_super.
DR Pfam; PF03098; An_peroxidase_1.
DR PRINTS; PR00457; ANPEROXIDASE.
DR PROSITE; PS00435; PEROXIDASE_1; FALSE NEG.
DR PROSITE; PS00436; PEROXIDASE_2; FALSE NEG.
DR PROSITE; PS0292; PEROXIDASE_3; 1.
KW Glycoprotein; Heme; Hydrogen peroxide; Iron; Oxidoreductase;

KW Peroxidase; Signal.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 690 Peroxidase.
FT ACT_SITE 185 331 Proton acceptor (By similarity).
FT ACT_SITE 331 331 Charge stabilization (By similarity).
FT METAL 437 437 Iron (heme axial ligand) (By similarity).
FT CARBOHYD 310 310 N-linked (GlcNAc...) (Potential).
FT CONFLICT 584 584 T -> A (in Ref. 3 and 5).
FT CONFLICT 678 678 P -> L (in Ref. 3 and 5).
SQ SEQUENCE 690 AA; 76733 MW; 4B16CE5411EB73C0 CRC64;

Query Match 51.9%; Score 42; DB 1; Length 690;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSPRTSPQN 14
:|||||: :|||
Db 55 VIGNSLPSPAPQN 68

RESULT 25
Q9LSE3 PRELIMINARY; PRT; 772 AA.
AC Q9LSE3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE EMB|CAA68822.1 (Putative RING zinc finger protein).
GN NameAt3926730;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL clones.";
RN [2]
RP SEQUENCE FROM N.A.
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RA Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AB026648; BAB01736.1; -;
DR EMBL; AY074325; AAL67021.1; -;
DR EMBL; BT003004; AAO22812.1; -;
DR HSSP; P38398; 1JM7.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.

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DR GO:0008270; F:zinc ion binding; IEA.
DR GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00097; zf-C3HC4_1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 772 AA; 85232 MW; B42710EPE868C45 CRC64;

Query Match 51.9%; Score 42; DB 2; Length 772;
Best Local Similarity 61.5%; Pred. No. 3.9e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LGNSSPRTQSPON 14
DB 667 LGNSAPISSSPPN 679

RESULT 26
Q6BY30 PRELIMINARY; PRT; 901 AA.
AC Q6BY30;
DT 25-OCT-2004 (TREMELrel. 28, Created)
DT 25-OCT-2004 (TREMELrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMELrel. 28, Last annotation update)
DE Debaryomyces hansenii chromosome A of strain CBS767 of Debaryomyces hansenii.
DE hansenii.
GN ORFNames=DEHA0A1321g;
OS Debaryomyces hansenii CBS767.
OC Eukaryota; Fungi; Ascomycota; Saccharomycetaceae; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OX NCBI_TaxID=284592;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E., Goffard N., Frangoul L., Aglie M., Anthouard V., Babour A., Barbé V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boissame A., Boyer J., Cattellio L., Confanioleri F., de Daruvar A., Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koziel R., Lemaire M., Lesur I., Ma L., Muller H., Nicaud J.M., Nikolski M., Ostas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B., Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Wincker P., Souciet J.L.;
RA Nature 430:35-44(2004).
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Contains 1 Zn(2)-Cys(6) fungal-type binuclear cluster domain.
DR EMBL; CR382133; CAG84866.1; -.
DR GO:0005634; C:nucleus; IEA.
DR GO:0003700; F:transcription factor activity; IEA.
DR GO:0008270; F:zinc ion binding; IEA.
DR GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO:0006350; P:transcription; IEA.
DR InterPro; IPR007219; Fungal_trans.
DR InterPro; IPR001138; Fungi_trscrp_N.
DR Pfam; PF04082; Fungal_trans; 1.
DR Pfam; PF00172; Zn_clus; 1.
DR PRINTS; PR00054; FUNGALZNCYS.
DR SMART; SM00066; GAL4; 1.

DR PROSITE; PS00463; ZN2_CY6_FUNGAL_1; 1.
DR PROSITE; PS00448; ZN2_CY6_FUNGAL_2; 1.
DR DNA-binding; Metal-binding; Nuclear protein; Transcription;
DR Transcription regulation; Zinc.
SQ SEQUENCE 901 AA; 103042 MW; 80DE2AACBED76253 CRC64;

Query Match 51.9%; Score 42; DB 2; Length 901;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GNSSPRTQSPON 14
DB 16 GNNHPRTIYPQN 27

RESULT 27
SUUR_DROER STANDARD; PRT; 962 AA.
AC P59597;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Suppressor of Underreplication protein.
GN Name=SUUR;
OS Drosophila erecta (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7220;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Yurlova A., Belyakin S.N., Makunin I.V., Zhimulev I.F.;
RT "Cloning of Drosophila erecta SuUR gene";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Required for underreplication of DNA, which is found in many late replicating euchromatic regions of salivary gland polytene chromosomes. Controls chromatin organization in polytene chromosomes (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear. Binds to polytene chromosomes from salivary glands; localized at late-replicating intercalary heterochromatin and pericentric heterochromatin. Colocalizes with many Polycomb Group proteins binding sites on polytene chromosomes (By similarity).
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DR EMBL; AJ539550; CAD62567.1; -.
DR FlyBase; FBgn0045001; Dere\SuUR.
DR InterPro; IPR000637; A+T hook.
DR InterPro; IPR000330; SNF2_N.
DR Pfam; PF00176; SNF2_N; 1.
DR SMART; SM00384; AT_hook; 1.
DR Chromatin regulator; Developmental protein; Nuclear protein.
SQ SEQUENCE 962 AA; 107466 MW; C79A4E2BC52EF9D6 CRC64;

Query Match 51.9%; Score 42; DB 1; Length 962;
Best Local Similarity 57.1%; Pred. No. 5e+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 LGNSSPRTQSPON 15
DB 367 LVNKSPTKSKKC 380

RESULT 28
Q23863

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ID Q23863 PRELIMINARY; PRT; 2150 AA.
AC Q23863;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Histidine kinase A.
GN Name=dhka;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Metazoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RC SEQUENCE FROM N.A.
PC STRAIN=Ax4;
RX MEDLINE=96324397; PubMed=8670894;
RA Wang N., Shaulsky G., Escalante R., Loomis W.F.;
RT "A two-component histidine kinase gene that functions in Dictyostelium
RT development.";
RL EMOB J. 15:3890-3898(1996).
CC -I- SIMILARITY: Contains 1 histidine kinase domain.
DR EMBL; U42597; AAC47300.1; -.
DR PIR; S71629; S71629.
DR HSSP; P39928; 10XK.
DR DictyBase; DB0215354; dhka.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . .); IEA.
DR InterPro; IPR003594; AtPbind_Arpase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR006189; CHASE.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR003661; His_kinA_N.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR001789; Response_reg.
DR InterPro; IPR011051; RmlC_like_cupin.
DR Pfam; PF03924; CHASE; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; Hiska; 1.
DR Pfam; PF00072; Response_reg; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; Hiska; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS0839; CHASE; 1.
DR PROSITE; PS0109; HIS_KIN; 1.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
KW Kinase; Phosphorylation; Sensory transduction.
SQ SEQUENCE 2150 AA; 239662 MW; 1FC3F63CE0336FA2 CRC64;

Query Match 51.9%; Score 42; DB 2; Length 2150;
Best Local Similarity 53.8%; Pred. No. 1.2e+03;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 3 GNSSPRTQSPONC 15
DB 345 GNSSPRNGSGNC 357

RESULT 29
OY Q7TPH6 PRELIMINARY; PRT; 4708 AA.
AC Q7TPH6;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DE Highwire.
GN Name=Phrl;
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
PC STRAIN=C57BL/6J;
RX PubMed=1472956; DOI=10.1128/MCB.24.3.1096-1105.2004;
RA Burgess R.W., Peterson K.A., Johnson M.J., Roix J.J., Welsh I.C.,
RA O'Brien T.P.;
RT "Evidence for a conserved function in synapse formation reveals Phrl
RT as a candidate gene for respiratory failure in newborn mice.";
RL Mol. Cell. Biol. 24:1096-1105(2004).
DR EMBL; AY325887; AAP8591.1; -.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR008938; ARM.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001298; Filamin.
DR InterPro; IPR009091; RCC1/BLIP-II.
DR InterPro; IPR000408; Reg_chrom_condens.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00415; RCC1; 1.
DR SMART; SM0184; RING; 1.
DR PROSITE; PS00150; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00194; FILAMIN_REPEAT; 1.
DR PROSITE; PS00626; RCC1_2; 1.
DR PROSITE; PS50012; RCC1_3; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 4708 AA; 517357 MW; B9B8717F81DFD5F8 CRC64;

Query Match 51.9%; Score 42; DB 2; Length 4708;
Best Local Similarity 66.7%; Pred. No. 2.9e+03;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 GNSSPRTQSPON 14
DB 2870 GASSPRSSSPQD 2881

RESULT 30
OY Q8YL47 PRELIMINARY; PRT; 148 AA.
AC Q8YL47;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Alr7088 protein.
GN OrderedLocusNames=alr7088;
OS Anabaena sp. (strain PCC 7120).
OG Plasmid pCC7120alpha.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003600; BAB78172.1; -.
DR PIR; AH2488; AH2488.
KW Complete proteome; Plasmid.
SQ SEQUENCE 148 AA; 16201 MW; 8956B9E2A0637911 CRC64;

Query Match 50.6%; Score 41; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Amorphaeae; Amorpha.
OK NCBI_TaxID=48131;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stem;
RA Liu W.-Z.; An L.-J.;
PL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC family.
DR EMBL; AF435968; AAL35216.1; -.
DR HSSP; P08659; 1LCI.
DR GO; GO:0016207; F:4-coumarate-CoA ligase activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR Pfam; PF00501; AMP-BINDING; 1.
DR PRINTS; PR00154; AMPBINDING.
DR PROSITE; PS00455; AMP_BINDING; 1.
KW Ligase.
SQ SEQUENCE 540 AA; 59315 MW; F399023E92440B79 CRC64;

Query Match 50.6%; Score 41; DB 2; Length 540;
Best Local Similarity 61.5%; Pred. No. 3.8e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 GNSSPRTQSPQNC 15
||| ||| :
DB 374 GNSLPRNQSGEIC 386

RESULT 38
4CL2_TOBAC
ID 4CL2_TOBAC STANDARD; PRT; 542 AA.
AC O24146;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 4-coumarate-CoA ligase 2 (EC 6.2.1.12) (4CL 2) (4-coumaroyl-CoA
synthase 2).
GN Name=4CL2;
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96416441; PubMed=8819324; DOI=10.1104/pp.112.1.193;
RA Lee D.; Douglas C.J.;
RT "Two divergent members of a tobacco 4-coumarate:coenzyme A ligase
(4CL) gene family. cDNA structure, gene inheritance and expression,
and properties of recombinant proteins.";
RL Plant Physiol. 112:193-205(1996).
CC -!- CATALYTIC ACTIVITY: ATP + 4-coumarate + CoA = AMP + diphosphate +
4-coumaroyl-CoA.
CC -!- PATHWAY: Branch-point reactions between general phenylpropanoid
metabolism and pathways leading to various specific end products.
CC -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC family.
CC -----
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CC -----
CC EMBL; U50846; AAB18638.1; -.
DR PIR; T03789; T03789.
DR HSSP; P08659; 1LCI.
DR InterPro; IPR000873; AMP-bind.

DR Pfam; PF00501; AMP-binding; 1.
DR PRINTS; PR00154; AMPBINDING.
DR TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.
DR TIGRFAMs; TIGR01923; menE; 1.
DR PROSITE; PS00455; AMP_BINDING; 1.
KW Ligase; Multigene family; Phenylpropanoid metabolism.
SQ SEQUENCE 542 AA; 59479 MW; CB5579AEDFCFC003 CRC64;

Query Match 50.6%; Score 41; DB 1; Length 542;
Best Local Similarity 61.5%; Pred. No. 3.8e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 GNSSPRTQSPQNC 15
||| ||| :
DB 377 GNSLPRNQSGEIC 389

RESULT 39
Q42943
ID Q42943 PRELIMINARY; PRT; 542 AA.
AC Q42943;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 4-coumarate:coenzyme A ligase (EC 6.2.1.12).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SRI;
RA Katayama Y.; Kawai S.; Morohoshi N.; Kajita S.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC family.
DR EMBL; D43773; BAA07828.1; -.
DR PIR; T02074; T02074.
DR HSSP; P08659; 1LCI.
DR GO; GO:0016207; F:4-coumarate-CoA ligase activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 1.
DR PRINTS; PR00154; AMPBINDING.
DR PROSITE; PS00455; AMP_BINDING; 1.
KW Ligase.
SQ SEQUENCE 542 AA; 59450 MW; C4EEFACCC4EA0650 CRC64;

Query Match 50.6%; Score 41; DB 2; Length 542;
Best Local Similarity 61.5%; Pred. No. 3.8e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 GNSSPRTQSPQNC 15
||| ||| :
DB 377 GNSLPRNQSGEIC 389

RESULT 40
Q6TUF8
ID Q6TUF8 PRELIMINARY; PRT; 556 AA.
AC Q6TUF8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LRRGT00086.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.


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RC STRAIN=Sprague-Dawley;
RA Xu C.S., Chang C.F., Han H.P., Wang G.P., Chai L.O., Yuan J.Y.,
RA Yang K.J., Zhao L.F., Ma H., Wang L., Wang S.F., Xing X.K., Shen G.M.,
RA Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY387072; AAQ91042.1; -.
DR HSP; P00750; IASH.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0007596; F:blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001177; Apple.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR01254; Peptidase S1.
DR InterPro; IPR09003; Pept_Ser_Cys.
DR Pfam; PF00024; PAN; 3.
DR PRINTS; PR00005; APLEDOMAIN.
DR SMART; SM00223; APPLE; 3.
DR SMART; SM00020; TRYP_SPE; 1.
DR PROSITE; PS00495; APPLE; 1.
DR PROSITE; PS00948; PAN; 2.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 556 AA; 62989 MW; 0A15BCA5580E2558 CRC64;

Query Match 50.6%; Score 41; DB 2; Length 556;
Best Local Similarity 58.3%; Pred. No. 4e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 LGSSPRTQSPQ 13
||:|||||:|:|
DB 392 LGSSPSTETPK 403

RESULT 41
QSPR2
ID Q8PIR2 PRELIMINARY; PRT; 577 AA.
AC Q8PIR2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Extracellular serine protease.
GN OrderedLocustNames=XAC2833;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=2202145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Cimarotte G., Cannavaro F., Cardoso J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locall E.C., Machado M.A., Madeiro A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities."
RL Nature 417:459-463(2002).
CC -!- SIMILARITY: Belongs to peptidase family S8.

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DR EMBL; AE011924; AAM37678.1; -.
DR HSP; P00780; ICSE.
DR GO; GO:0004269; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR000209; Pept_S8_S53.
DR InterPro; IPR002884; PrptotnConvertp.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF01483; P_protein; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR ProDom; PD000717; PrptotnConvertp; 1.
DR PROSITE; PS00136; SUBTILASE_ASP; 1.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; UNKNOWN 1.
KW Complete proteome; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 577 AA; 61529 MW; 33777969B1BC37E CRC64;

Query Match 50.6%; Score 41; DB 2; Length 577;
Best Local Similarity 58.3%; Pred. No. 4.1e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GNSSPRTQSPQN 14
||:|||||:|:|
DB 330 GNNRDRTRAPQN 341

RESULT 42
CDYL MOUSE
ID --CDYL MOUSE STANDARD; PRT; 593 AA.
AC Q9WTK2;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chromodomain Y-like protein (CDY-like).
GN Name=Cdy1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=99206615; PubMed=10192397; DOI=10.1038/7771;
RA Lahn B.T., Page D.C.;
RA "Retroposition of autosomal mRNA yielded testis-specific gene family on human Y chromosome."
RL Nat. Genet. 21:429-433(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Maman A., Rodriguez S., Sanchez A.,
RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Smerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed as 2 transcripts: a ubiquitous

```



```
CC transcript and a highly expressed testis-specific transcript.
CC -I- SIMILARITY: Contains 1 chromo domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF081260; AAD22736.1; -
DR EMBL; AF081261; AAD22737.1; -
DR EMBL; BC055103; AAHS5103.1; -
DR HSSP; F23197; IGW.
DR MGD; MGI:133956; Cdy1.
DR InterPro; IPR000953; Chromo.
DR InterPro; IPR001753; EnCoA_hydrase.
DR Pfam; PF00385; Chromo; 1.
DR Pfam; PF00378; ECH; 1.
DR PROSITE; PS00598; CHROMO_1; 1.
DR PROSITE; PS00013; CHROMO_2; 1.
KW Nuclear protein.
FT DOMAIN 56 116 Chromo.
SQ SEQUENCE 593 AA; 65211 MW; 470D5B97D7E52CCA CRC64;
SQ
Query Match 50.6%; Score 41; DB 1; Length 593;
Best Local Similarity 50.0%; Pred. No. 4.2e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 LGNSSPRTQSPQNC 15
:|:|:|:|:|:|
DB 3 IGNSQPNQOEALQC 16

RESULT 43
Q64033 PRELIMINARY; PRT; 599 AA.
AC Q64033;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Antigen LEC-A.
GN Name=gag;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94374432; PubMed=8088336;
RA de Bergeyck V., De Plaen E., Chomez P., Boon T., Van Pel A.;
RT "An intracisternal A-particle sequence codes for an antigen recognized
RT by syngeneic cytolytic T lymphocytes on a mouse spontaneous
RT leukemia.";
RL Eur. J. Immunol. 24:2203-2212(1994).
DR EMBL; S74315; AAB31958.1; -
DR PIR; I53395; I53395.
DR HSSP; P11284; LDSV.
DR GO; GO:0003676; F nucleic acid binding; IEA.
DR GO; GO:0016032; P viral life cycle; IEA.
DR InterPro; IPR000721; Gag_p24.
DR InterPro; IPR008916; Retrov_capsid_C.
DR InterPro; IPR008919; Retrov_capsid_N.
DR Pfam; PF00607; Gag_p24; 1.
DR Pfam; PF00098; zf-CCHC; 1.
DR PRINTS; PR00939; C2HCZNFINGER.
DR SMART; SM00343; Znf_C2HC; 2.
DR PROSITE; PS0158; ZF_CCHC; 1.
SQ SEQUENCE 599 AA; 57365 MW; 1EEB09B2F0B94CD6 CRC64;
SQ
Query Match 50.6%; Score 41; DB 2; Length 599;
Best Local Similarity 50.0%; Pred. No. 4.2e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
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```
Best Local Similarity 63.6%; Pred. No. 4.3e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 GNSSPRTQSPQ 13
|:|:|:|:|:|
DB 556 GSSGPRSQGPQ 566

RESULT 44
Q96DR7 PRELIMINARY; PRT; 871 AA.
ID Q96DR7
AC Q96DR7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Putative SH3 domain-containing guanine exchange factor SGEF.
GN Name=SGEF;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Prostate cancer;
RX MEDLINE=22583556; PubMed=12697679; DOI=10.1210/en.2002-220984;
RA Qi H., Fournier A., Grenier J., Fillion C., Labrie Y., Labrie C.;
RT "Isolation of the novel human guanine nucleotide exchange factor Src
RT homology 3 domain-containing guanine nucleotide exchange factor (SGEF)
RT and of C-terminal SGEF, an N-terminally truncated form of SGEF, the
RT expression of which is regulated by androgen in prostate cancer
RT cells.";
RL Endocrinology 144:1742-1752(2003).
CC -I- SIMILARITY: Contains 1 PH domain.
CC -I- SIMILARITY: Contains 1 SH3 domain.
DR EMBL; AF415175; AAL27001.1; -
DR HSSP; P19878; 1K4U.
DR InterPro; IPR001849; PH.
DR InterPro; IPR00219; RhoGEF.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhoGEF; 1.
DR Pfam; PF00018; SH3_1; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhoGEF; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50010; DH_2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50002; SH3; 1.
KW SH3 domain.
SQ SEQUENCE 871 AA; 97402 MW; 326080B5A2999F60 CRC64;
SQ
Query Match 50.6%; Score 41; DB 2; Length 871;
Best Local Similarity 64.3%; Pred. No. 6.5e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LGNSSPRTQSPQN 14
|:|:|:|:|:|
DB 29 LLGRSKPRQSQYQS 42

RESULT 45
Q6AZ96 PRELIMINARY; PRT; 871 AA.
ID Q6AZ96
AC Q6AZ96;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE DKF2P434D146 protein.
GN Name=SGEF;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield V.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Contains 1 SH3 domain.
DR EMBL; BC078655; AAT78655.1; -.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011036; PH related.
DR InterPro; IPR000219; RhGEF.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR011511; SH3_2.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhGEF; 1.
DR Pfam; PF00018; SH3_1; 1.
DR Pfam; PF07653; SH3_2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhGEF; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50010; DH 2; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
DR PROSITE; PS50002; SH3; 1.
DR SH3 domain.
KW SH3 domain.
SQ SEQUENCE 871 AA; 97347 MW; 43BB87127A05144B CRC64;

Query Match 50.6%; Score 41; DB 2; Length 871;
Best Local Similarity 64.3%; Pred. No. 6.5e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSPQN 14
Db 29 LLGSKRPQSQS 42

RESULT 46
Q6Q8Q8 ID Q6Q8Q8 PRELIMINARY; PRT; 871 AA.
AC Q6Q8Q8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SH3-containing guanine nucleotide exchange factor.
GN Name=SGEF;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX PubMed=15133129;
RA Ellerbroek S.M., Wennerberg K., Arthur W.T., Dunty J.M., Bowman D.R.,
RA DeMali K.A., Der C., Burridge K.;
RT "SGEF, a RhG Guanine Nucleotide Exchange Factor that Stimulates
RL Mol. Biol. Cell 15:3309-3319(2004).
CC -I- SIMILARITY: Contains 1 PH domain.
CC -I- SIMILARITY: Contains 1 SH3 domain.
DR EMBL; AY552599; AAS59842.1; -.
DR HSP; P19878; IK4U.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; RhGEF.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhGEF; 1.
DR Pfam; PF00018; SH3_1; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhGEF; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50010; DH 2; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
DR PROSITE; PS50002; SH3; 1.
DR SH3 domain.
KW SH3 domain.
SQ SEQUENCE 871 AA; 97333 MW; 28D081A4A3898B61 CRC64;

Query Match 50.6%; Score 41; DB 2; Length 871;
Best Local Similarity 64.3%; Pred. No. 6.5e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSPQN 14
Db 29 LLGSKRPQSQS 42

RESULT 47
Q6DRCS ID Q6DRCS PRELIMINARY; PRT; 1014 AA.
AC Q6DRCS;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE D3SI06E-like.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15256591; DOI=10.1073/pnas.0403929101;
RA Amsterdam A., Nissen R.M., Sun Z., Swindell E.C., Farrington S.,
RA Hopkins N.;
RT "Identification of 315 genes essential for early zebrafish
RL development.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:12792-12797(2004).
DR EMBL; AY648834; AAT68152.1; -.
SQ SEQUENCE 1014 AA; 112531 MW; 14BCCCA22B2BC5A6 CRC64;

Query Match 50.6%; Score 41; DB 2; Length 1014;
Best Local Similarity 57.1%; Pred. No. 7.7e+02;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 LGNSSPRTQSPQNC 15
Db 19 LGKSKRNASPGNC 32

RESULT 48
FSH_DROME
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX PubMed=15133129;
RA Ellerbroek S.M., Wennerberg K., Arthur W.T., Dunty J.M., Bowman D.R.,
RA DeMali K.A., Der C., Burridge K.;
RT "SGEF, a RhG Guanine Nucleotide Exchange Factor that Stimulates
RL Mol. Biol. Cell 15:3309-3319(2004).
CC -I- SIMILARITY: Contains 1 PH domain.
CC -I- SIMILARITY: Contains 1 SH3 domain.
DR EMBL; AY552599; AAS59842.1; -.
DR HSP; P19878; IK4U.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; RhGEF.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhGEF; 1.
DR Pfam; PF00018; SH3_1; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhGEF; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50010; DH 2; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
DR PROSITE; PS50002; SH3; 1.
DR SH3 domain.
KW SH3 domain.
SQ SEQUENCE 871 AA; 97333 MW; 28D081A4A3898B61 CRC64;

Query Match 50.6%; Score 41; DB 2; Length 871;
Best Local Similarity 64.3%; Pred. No. 6.5e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSPQN 14
Db 29 LLGSKRPQSQS 42

RESULT 47
Q6DRCS ID Q6DRCS PRELIMINARY; PRT; 1014 AA.
AC Q6DRCS;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE D3SI06E-like.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15256591; DOI=10.1073/pnas.0403929101;
RA Amsterdam A., Nissen R.M., Sun Z., Swindell E.C., Farrington S.,
RA Hopkins N.;
RT "Identification of 315 genes essential for early zebrafish
RL development.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:12792-12797(2004).
DR EMBL; AY648834; AAT68152.1; -.
SQ SEQUENCE 1014 AA; 112531 MW; 14BCCCA22B2BC5A6 CRC64;

Query Match 50.6%; Score 41; DB 2; Length 1014;
Best Local Similarity 57.1%; Pred. No. 7.7e+02;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 LGNSSPRTQSPQNC 15
Db 19 LGKSKRNASPGNC 32

RESULT 48
FSH_DROME
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PSH DROME STANDARD; PRT; 2038 AA.

AC P13709; P13710; 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Female sterile homeotic protein (Fragile-chorion membrane protein).

GN Name=fs(1)h; Synonyms=fs(1)h; ORFNames=CG225252;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

FN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89276730; PubMed=2567251;

RA Haynes S.R., Mozer B.A., Bhatia-Dey N., Dawid I.B.;

RT "The Drosophila fish locus, a maternal effect homeotic gene, encodes

RT apparent membrane proteins.";

RL Dev. Biol. 134:246-257(1989).

CC -!- FUNCTION: Required maternally for proper expression of other

CC homeotic genes involved in pattern formation, such as Ubx.

CC -!- SIMILARITY: Contains 2 bromodomains.

CC -!- SIMILARITY: Contains 1 ET domain.

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CC -----

EMBL; M23221; AAA28540.1; -;

EMBL; M23222; AAA28541.1; ALT TERM.

DR EMBL; M15762; AAA70424.1; -;

DR EMBL; M15763; AAA70423.1; -;

DR EMBL; M15764; AAA70422.1; -;

DR F01; A43742; A43742.

DR HSP; Q92830; 1F68.

DR FlyBase; FBgn004656; fs(1)h.

DR InterPro; IPR001487; Bromodomain.

DR Pfam; PF00439; Bromodomain; 2.

DR PRINTS; PR00503; BROMODOMAIN.

DR SMART; SM00297; BROMO; 2.

DR PROSITE; PS00633; BROMODOMAIN 1; 2.

DR PROSITE; PS50014; BROMODOMAIN 2; 2.

KW Bromodomain; Developmental protein; Repeat; Transmembrane.

FT DOMAIN 51 123

FT DOMAIN 495 567

FT DOMAIN 945 1106

FT TRANSMEM 330 350

FT TRANSMEM 451 471

FT TRANSMEM 750 770

FT TRANSMEM 790 810

FT TRANSMEM 816 830

FT TRANSMEM 874 894

FT TRANSMEM 1731 1751

FT TRANSMEM 1939 1959

FT VARIANT 909 909

FT VARIANT 1022 1022

FT VARIANT 2038 AA; 205332 MW; 849E0706D50A0098 CRC64;

FT SEQUENCE

Query Match 50.6%; Score 41; DB 1; Length 2038;

Best Local Similarity 66.7%; Pred. No. 1.7e+03;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GNSSPRTQSPQN 14

DB 1985 GOSPPAQSPQD 1996

RESULT 49

Q9W3L3

ID AC Q9W3L3

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE CG2252-PB.

GN Name=fs(1)h; ORFNames=CG225252;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

FN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brannon R.C., Rogers J.H., Blazek R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Fofor C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,

RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Liakop P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Mount D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,

RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J., Ye J.,

RA Williams S.M., Woodruff, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

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RL Science 287:2185-2195(2000).

RP SEQUENCE FROM N.A.

RX MEDLINE=22426065; PubMed=12537568;

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RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,

RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;

RT "Finishing a whole-genome shotgun. Release 3 of the Drosophila

RT melanogaster euchromatic genome sequence.";

RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RP SEQUENCE FROM N.A.

RX MEDLINE=22426070; PubMed=12537573;

RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,

RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,

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RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berwan B.P.,
RA Bettencourt B.R., Celisner S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.N., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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DR HSSP; Q92830; 1F68.
DR Interact; Q9W3L3; -.
DR FlyBase; FBgn004656; fs(1)h.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR002173; PfkB.
DR Pfam; PF00439; Bromodomain; 2.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00297; BROMO; 2.
DR PROSITE; PS00633; BROMODOMAIN 1; 2.
DR PROSITE; PS50014; BROMODOMAIN 2; 2.
DR PROSITE; PS00583; PFKB KINASES 1; UNKNOWN 1.
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Best Local Similarity 66.7%; Pred. No. 1.7e+03;
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DT 01-FEB-1995 (Rel. 31, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=83355;
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RC TISSUE=Oocyte;
RX MEDLINE=96180312; PubMed=8597594; DOI=10.1016/0167-4781(95)00228-6;
RA Komatsu N., Hiraoka Y., Shiozawa M., Ogawa M., Aiso S.;
RT "Cloning and expression of Xenopus laevis xSox12 cDNA.";
RL Biochim. Biophys. Acta 1305:117-119(1996).
RN [2]
RP SEQUENCE OF 306-359 FROM N.A.
RX MEDLINE=92310993; PubMed=1614875;
RA Denny P., Swift S., Brand N., Dabhadre N., Barton P., Ashworth A.;
RT "A conserved family of genes related to the testis determining gene,
RT SRY.";
RL Nucleic Acids Res. 20:2887-2887(1992).

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CC -i- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -i- SIMILARITY: Contains 1 HMG box domain.
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CC HSSP; P35710; 1L11.
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CC PROSITE; PS50118; HMG_BOX 2; 1.
KW DNA-binding, Nuclear protein. HMG box.
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Job time : 174 secs

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OM protein - protein search, using sw model

Run on: August 25, 2005, 11:35:23 ; Search time 41 Seconds
(without alignments)
27.311 Million cell updates/sec

Title: US-10-803-541-2

Perfect score: 81

Sequence: 1 LLGNSSPRTQSPQNC 15

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	515	2	US-08-705-660-46
2	81	100.0	515	3	US-08-989-045-46
3	81	100.0	515	4	US-09-315-355A-46
4	81	100.0	664	4	US-09-538-092-838
5	44	54.3	83	4	US-09-621-976-4157
6	44	54.3	970	4	US-09-538-092-664
7	42	51.9	88	4	US-09-621-976-3949
8	42	51.9	88	4	US-09-621-976-5346
9	42	51.9	164	4	US-09-252-991A-30496
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11	41	50.6	10	2	US-08-429-964-16
12	41	50.6	10	5	PTC-US93-08062-16
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87	38	46.9	305	4	US-10-023-894-7
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ALIGNMENTS

RESULT 1
US-08-705-660-46
; Sequence 46, Application US/08705660
; Patent No. 5858683
; GENERAL INFORMATION:
; APPLICANT: KEESEE, SUSAN
; APPLICANT: OBAR, ROBERT
; APPLICANT: WU, YING-JYE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; DETECTION OF CERVICAL CANCER
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,660
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: GREENHALGH, DUNCAN A
; REGISTRATION NUMBER: 38,678
; REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; MOLECULE TYPE: peptide
; US-08-705-660-46

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; GENERAL INFORMATION:
; APPLICANT: KEESEE, SUSAN
; APPLICANT: OBAR, ROBERT
; APPLICANT: WU, YING-JYE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; DETECTION OF CERVICAL CANCER
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,045
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: GREENHALGH, DUNCAN A
; REGISTRATION NUMBER: 38,678
; REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; MOLECULE TYPE: peptide
; US-08-989-045-46

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Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 498 LLGSSPRTQSPQNC 512

RESULT 3
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; Sequence 46, Application US/09315355A
; Patent No. 6803189
; GENERAL INFORMATION:
; APPLICANT: KEESEE, SUSAN
; APPLICANT: OBAR, ROBERT
; APPLICANT: WU, YING-JYE
; TITLE OF INVENTION: Methods for the Detection of Cervical Cancer
; FILE REFERENCE: MTP-023DV2
; CURRENT APPLICATION NUMBER: US/09/315,355A
; CURRENT FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: US 08/989,045
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: US 08/705,660
; PRIOR FILING DATE: 1996-08-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
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; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-315-355A-46

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RESULT 4
US-09-538-092-838
; Sequence 838, Application US/09538092
; Patent No. 6753314
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; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
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; NAME/KEY: misc feature
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Best Local Similarity 100.0%; Pred. No. 4.7e-05;
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QY 1 LLGNSPRTQSPQNC 15
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RESULT 5
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; Sequence 4157, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4157
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Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLGNSPRTQSPON 14
Db 13 LLGSSSPPTASQN 26

RESULT 6
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; Sequence 664, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
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; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 664
; LENGTH: 970
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number YNL118C
;
US-09-538-092-664
Query Match 54.3%; Score 44; DB 4; Length 970;
Best Local Similarity 75.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GNSSPRTQSPON 14
Db 595 GKSSPSTQSQNW 606

RESULT 7
US-09-621-976-3949
; Sequence 3949, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3949
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -37...-1
; NAME/KEY: UNSURE
; LOCATION: 10
; OTHER INFORMATION: Xaa = Arg,Thr
US-09-621-976-3949
Query Match 51.9%; Score 42; DB 4; Length 88;
Best Local Similarity 64.3%; Pred. No. 11;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLGNSPRTQSPON 14
Db 27 LLGSSSPPTLASQN 40

RESULT 8
US-09-621-976-5346
; Sequence 5346, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
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; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pgm
; SEQ ID NO 5346
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SIGNAL
; LOCATION: -37...-1
; NAME/KEY: UNSURE
; LOCATION: 10
; OTHER INFORMATION: Xaa = Arg, Thr
US-09-621-976-5346

Query Match          51.9%; Score 42; DB 4; Length 89;
Best Local Similarity 64.3%; Pred. No. 12;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGSSPRTQSPQN 14
Db 27 LLGSSPPTLASQN 40

RESULT 9
US-09-252-991A-30496
; Sequence 30496, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30496
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30496

Query Match          51.9%; Score 42; DB 4; Length 164;
Best Local Similarity 63.6%; Pred. No. 23;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 SSPTQSPQNC 15
Db 22 SNPRHQEQSC 32

RESULT 10
PCT-US96-03916-19
; Sequence 19, Application PC/TUS9603916
; GENERAL INFORMATION:
; APPLICANT: Wild, Martha A.
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/03916
; FILING DATE: 23-MAR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,597
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39116-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-03916-19

Query Match          51.9%; Score 42; DB 5; Length 177;
Best Local Similarity 53.3%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 LLGSSPRTQSPQNC 15
Db 5 LLNRGSPRLNPPKC 19

RESULT 11
US-08-429-964-16
; Sequence 16, Application US/08429964
; Patent No. 5962243
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: GOLDSTEIN, JOSEPH L.
; APPLICANT: REISS, YUVAL
; APPLICANT: JAMES, GUY L.
; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P. O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/429,964
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/021,625
; FILING DATE: 16-FEB-1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/822,011
; FILING DATE: ABANDONED
; CLASSIFICATION: 435
; APPLICATION NUMBER: PCT/US/91/02650
; FILING DATE: 18-APR-1991
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/615,715

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; FILING DATE: 20-NOV-1990
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/510,706
; FILING DATE: 18-APR-1990 (ABANDONED)
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PARKER, DAVID L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSD:432/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 785-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-423-964-16

Query Match 50.6%; Score 41; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 TQSPQNC 15
Db 1 TQSPQNC 7

RESULT 12
PCT-US93-08062-16
; Sequence 16, Application PC/TUS9308062
; GENERAL INFORMATION:
; APPLICANT:
; SEQUENCE CHARACTERISTICS: BROWN, MICHAEL S.
; SEQUENCE CHARACTERISTICS: GOLDSTEIN, JOSEPH L.
; SEQUENCE CHARACTERISTICS: REISS, YUVAL
; SEQUENCE CHARACTERISTICS: MARSTERS, JR., JAMES C.
; ADDRESSES: METHODS AND COMPOSITIONS FOR
; ADDRESS: THE IDENTIFICATION,
; ADDRESS: CHARACTERIZATION AND
; ADDRESS: INHIBITION OF
; ADDRESS: FARNESYLTRANSFERASE
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK/ASKII
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08062
; FILING DATE: AUGUST 24, 1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/935,087
; FILING DATE: 24 AUGUST 1992 (24.08.92)
; NAME: UNKNOWN
; ATTORNEY/AGENT INFORMATION:
; NAME: PARKER, DAVID L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSD377PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 512-474-7577

; TELEX: NOT APPLICABLE
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US93-08062-16

Query Match 50.6%; Score 41; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 TQSPQNC 15
Db 1 TQSPQNC 7

RESULT 13
US-09-270-767-45686
; Sequence 45686, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 45686
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45686

Query Match 49.4%; Score 40; DB 4; Length 136;
Best Local Similarity 46.7%; Pred. No. 39;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 1 LLGNSSPRTQSPQNC 15
Db 11 LLTNTDPRTRTESRC 25

RESULT 14
US-09-949-016-7849
; Sequence 7849, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7849
; LENGTH: 1031
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7849

Query Match 49.4%; Score 40; DB 4; Length 1031;

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Best Local Similarity 53.8%; Pred. No. 3.6e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSPRTQSPQ 13
Db 225 LTGESEPQTRSPF 237

RESULT 15
US-09-252-991A-25786
; Sequence 25786, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25786
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25786

Query Match 48.1%; Score 39; DB 4; Length 144;
Best Local Similarity 53.8%; Pred. No. 60;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GNSPRTQSPQNC 15
Db 96 GSTSPTTASAPNC 108

RESULT 16
US-07-800-364B-14
; Sequence 14, Application US/07800364B
; Patent No. 5688678
; GENERAL INFORMATION:
; APPLICANT: Hewick, Rodney M.
; APPLICANT: Wang, Jack H.
; APPLICANT: Wozney, John M.
; APPLICANT: Celeste, Anthony J.
; TITLE OF INVENTION: Bone and Cartilage Inductive Proteins
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/800,364B
; FILING DATE: 26-NOV-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI 5182A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-5851
; TELEFAX: 617-876-5851

```

```

; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-800-364B-14

Query Match 48.1%; Score 39; DB 1; Length 281;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSPRTQSP 12
Db 114 LLGORAPRSQOP 125

RESULT 17
US-07-989-847-12
; Sequence 12, Application US/07989847
; Patent No. 5866364
; GENERAL INFORMATION:
; APPLICANT: Israel, David
; APPLICANT: Wolfman, Neil M.
; TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
; TITLE OF INVENTION: Heterodimers, Compositions and Methods of Use.
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140-2387
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,847
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI-5192B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-989-847-12

Query Match 48.1%; Score 39; DB 2; Length 281;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSPRTQSP 12
Db 114 LLGORAPRSQOP 125

RESULT 18
US-08-469-411-12
; Sequence 12, Application US/08469411
; Patent No. 6190880
; GENERAL INFORMATION:
; APPLICANT: Israel, David

```

;; Wolfman, Neil M.
;; TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
;; NUMBER OF SEQUENCES: 30
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
;; STREET: 87 CambridgePark Drive
;; CITY: Cambridge
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02140-2387
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Tape
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/469,411
;; FILING DATE: 06-Jun-1995
;; CLASSIFICATION: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kapinos, Ellen J.
;; REGISTRATION NUMBER: 32,245
;; REFERENCE/DOCKET NUMBER: GI-5192B-CON
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-498-8622
;; TELEFAX: 617-876-5851
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-08-469-411-12
Query Match 48.1%; Score 39; DB 3; Length 281;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 LLGNSPRTQSP 12
Db 114 LLGORAPRSQP 125
RESULT 19
US-09-601A-12
; Sequence 12, Application US/09780601A
; Patent No. 6593109
; GENERAL INFORMATION:
; APPLICANT: Israel, David
; APPLICANT: Wolfman, Neil M.
; TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140-2387
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/780,601A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,411

;; FILING DATE: 06-Jun-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kapinos, Ellen J.
;; REGISTRATION NUMBER: 32,245
;; REFERENCE/DOCKET NUMBER: GI-5192B-CON
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-498-8622
;; TELEFAX: 617-876-5851
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 281 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-780-601A-12
Query Match 48.1%; Score 39; DB 4; Length 281;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 LLGNSPRTQSP 12
Db 114 LLGORAPRSQP 125
RESULT 20
PCT-US91-07635-6
; Sequence 6, Application PC/TUS9107635
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: RUEGER, DAVID C
; APPLICANT: KUBERASAMPATH, THANGAVEL
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBRAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/07635
; FILING DATE: 19911018
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-056PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 399 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-07635-6
Query Match 48.1%; Score 39; DB 5; Length 399;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 LLGNSPRTQSP 12
Db 232 LLGORAPRSQP 243

RESULT 21
US-07-841-646-29
; Sequence 29, Application US/07841646
; Patent No. 5266583
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/841.646
; FILING DATE: 19920221
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; APPLICATION NUMBER: US 621,849
; FILING DATE: 04-DEC-1990
; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990
; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990
; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; APPLICATION NUMBER: US 569,920
; FILING DATE: 20-AUG-1990
; APPLICATION NUMBER: US 483,913
; FILING DATE: 22-FEB-1990
; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-841-646-29
Query Match 48.1%; Score 39; DB 1; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 LLGNSPRTQSP 12
Db 235 LLQRAPRSQOP 246
RESULT 22
US-07-901-703-11
; Sequence 11, Application US/07901703
; Patent No. 5344654
; GENERAL INFORMATION:
; APPLICANT: RUEGER, DAVID C
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; TITLE OF INVENTION: PROSTHETIC DEVICES HAVING ENHANCED
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: EXCHANGE PLACE, 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/901,703
; FILING DATE: 19920616
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: STK-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-901-703-11
Query Match 48.1%; Score 39; DB 1; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 LLGNSPRTQSP 12

Db 235 LLQAPRSQP 246
||| :||:|
FILING DATE: 15-AUG-1988
PRIOR APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-147-023-29

Query Match 48.1%; Score 39; DB 1; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSPRTQSP 12
||| :||:|
Db 235 LLQAPRSQP 246

RESULT 24
US-08-206-864-4
Sequence 4, Application US/08206864
Patent No. 5610021
GENERAL INFORMATION:
APPLICANT: RUEGER, DAVID C
APPLICANT: JONES, WILLIAM K
APPLICANT: TUCKER, RONALD F
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR/CREATIVE BIOMOLECULES,
ADDRESSEE: INC.
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206.864
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630

US-08-147-023-29
Sequence 29, Application US/08147023
Patent No. 5468845
GENERAL INFORMATION:
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H. L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,023
FILING DATE: 21-FEB-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-206-864-4

Query Match 48.1%; Score 39; DB 1; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSP 12
   ||| :||:|
Db 235 LLGQAPRSQQP 246

RESULT 25
US-08-278-729A-21
; Sequence 21, Application US/08278729A
; Patent No. 5650276
; GENERAL INFORMATION:
; APPLICANT: SMART, JOHN
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,729A
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 435
; NAME: PITCHER ESQ., EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-058CPFW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 435-9001
; TELEFAX: (508) 435-6951
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-278-729A-21

Query Match 48.1%; Score 39; DB 1; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSP 12
   ||| :||:|
Db 235 LLGQAPRSQQP 246

RESULT 26
US-08-480-528A-8
; Sequence 8, Application US/08480528A
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; Patent No. 5652118
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: OP3-INDUCED MORPHOGENESIS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,528A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON ESQ., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-076FW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7560
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-480-528A-8

Query Match 48.1%; Score 39; DB 1; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSP 12
   ||| :||:|
Db 235 LLGQAPRSQQP 246

RESULT 27
US-08-479-666-8
; Sequence 8, Application US/08479666
; Patent No. 5652337
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: OP3-INDUCED MORPHOGENESIS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,666
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FENTON Esq., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-076DV
TELEPHONE: (508) 435-9001
TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-666-8

Query Match 48.1%; Score 39; DB 1; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLGNSPRTQSP 12
|||:|:|
DB 235 LLGORAPRSQQP 246

RESULT 28
US-08-155-343A-21
Sequence 21, Application US/08155343A
Patent No. 5656593
GENERAL INFORMATION:
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: OPPERMANN, HERMAN
APPLICANT: COHEN, CHARLES M.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: MORPHOGENIC-INDUCED PERIODONTAL TISSUE
REGENERATION.
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,343A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FENTON Esq., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-067FW
TELEPHONE: (617) 248-7560
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-155-343A-21

Query Match 48.1%; Score 39; DB 1; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 LLGNSPRTQSP 12
|||:|:|
DB 235 LLGORAPRSQQP 246

RESULT 29
US-08-406-672-21
Sequence 21, Application US/08406672
Patent No. 56744844
GENERAL INFORMATION:
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: COHEN, CHARLES M.
APPLICANT: OPPERMANN, HERMAN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: TREATMENT TO PREVENT LOSS OF AND/OR
TITLE OF INVENTION: INCREASE BONE MASS IN METABOLIC BONE DISEASES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,672
FILING DATE: 20-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 752,857
FILING DATE: 30-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 667,274
FILING DATE: 11-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: FENTON Esq., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-060CN
TELEPHONE: (617) 248-7560
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-406-672-21

Query Match 48.1%; Score 39; DB 1; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 LLGNSPRTQSP 12
|||:|:|
DB 235 LLGORAPRSQQP 246

RESULT 30
US-08-643-563A-21
Sequence 21, Application US/08643563A

Patent No. 5707810
; GENERAL INFORMATION:
; APPLICANT: SMART, JOHN
; APPLICANT: OFFERMANN, HERMAN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,563A
; FILING DATE: 06-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: TWOMEY Esq., MICHAEL J.
; REGISTRATION NUMBER: 38,349
; REFERENCE/DOCKET NUMBER: CRP-058CN2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 435-9001
; TELEFAX: (508) 435-6951
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-643-563A-21

Query Match 48.1%; Score 39; DB 1; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 LLGNSSPRTQSP 12
||| :||:|
Db 235 LLGQAPRSQOP 246

RESULT 31
US-08-447-570-29
; Sequence 29, Application US/08447570
; Patent No. 5714589
; GENERAL INFORMATION:
; APPLICANT: OFFERMANN, HERMAN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,570
; FILING DATE: 21-FEB-1992
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,849
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 569,920
; FILING DATE: 20-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 483,913
; FILING DATE: 22-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-447-570-29

Query Match 48.1%; Score 39; DB 1; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 LLGNSSPRTQSP 12
||| :||:|
Db 235 LLGQAPRSQOP 246


```
RESULT 32
US-08-643-763A-21
; Sequence 21, Application US/08643763A
; Patent No. 5733878
; GENERAL INFORMATION:
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: MORPHOGENIC-INDUCED PERIODONTAL TISSUE
; TITLE OF INVENTION: REGENERATION.
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,763A
; FILING DATE: 06-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON Esq., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-067CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7560
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-643-763A-21

Query Match 48.1%; Score 39; DB 1; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLGNSPRTQSP 12
||| :||:|
Db 235 LLGQAPRSQQP 246

RESULT 33
US-08-462-623-21
; Sequence 21, Application US/08462623
; Patent No. 5739107
; GENERAL INFORMATION:
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: CHARETTE, MARC F.
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: PANG, ROY H.L.
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: SMART, JOHN E.
; TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL
; TITLE OF INVENTION: ULCERS.
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
```

```
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,623
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/445,882
; FILING DATE: 22-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON Esq., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-074CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 435-9001
; TELEFAX: (508) 435-6951
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-623-21

Query Match 48.1%; Score 39; DB 1; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLGNSPRTQSP 12
||| :||:|
Db 235 LLGQAPRSQQP 246

RESULT 34
US-08-451-953A-21
; Sequence 21, Application US/08451953A
; Patent No. 5741641
; GENERAL INFORMATION:
; APPLICANT: SMART, JOHN
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,953A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER Esq., EDMUND R.
```

; REGISTRATION NUMBER: 27,829
 ; REFERENCE/DOCKET NUMBER: CRP-058CN
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (508) 435-9001
 ; TELEFAX: (508) 435-6951
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 402 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-451-953A-21

Query Match 48.1%; Score 39; DB 1; Length 402;
 Best Local Similarity 58.3%; Pred. No. 1.9e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSP 12
 ||||:||||
 Db 235 LLGQAPRSQQP 246

RESULT 35
 US-08-459-346-6
 ; Sequence 6, Application US/08459346
 ; Patent No. 5834179

; GENERAL INFORMATION:
 ; APPLICANT: JONES, WILLIAM K
 ; APPLICANT: TUCKER, RONALD F
 ; APPLICANT: RUEGER, DAVID C
 ; APPLICANT: OPPERMANN, HERMANN
 ; APPLICANT: OZKAYNAK, ENGIN
 ; APPLICANT: KUBERASAMPATH, THANGAVEL
 ; TITLE OF INVENTION: NOVEL MORPHOGENIC PROTEIN COMPOSITIONS
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: PATENT ADMINISTRATOR/CREATIVE BIOMOLECULES,
 ; ADDRESSEE: INC.
 ; STREET: 35 SOUTH STREET
 ; CITY: HOPKINTON
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 01748

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/459,346
 ; FILING DATE:
 ; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/029,335
 ; FILING DATE: 04-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/971,091
 ; FILING DATE: 03-NOV-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/946,235
 ; FILING DATE: 16-SEP-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/938,336
 ; FILING DATE: 08-AUG-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/923,780
 ; FILING DATE: 31-JUL-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: FITCHER, EDWARD R
 ; REGISTRATION NUMBER: 27,829
 ; REFERENCE/DOCKET NUMBER: CRP-081CP
 ; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 402 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-459-346-6

Query Match 48.1%; Score 39; DB 2; Length 402;
 Best Local Similarity 58.3%; Pred. No. 1.9e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSP 12
 ||||:||||
 Db 235 LLGQAPRSQQP 246

RESULT 36
 US-08-445-468A-21
 ; Sequence 21, Application US/08445468A
 ; Patent No. 5849686

; GENERAL INFORMATION:
 ; APPLICANT: KUBERASAMPATH, THANGAVEL
 ; APPLICANT: RUEGER, DAVID C.
 ; APPLICANT: OPPERMANN, HERMAN
 ; APPLICANT: PANG, ROY H.L.
 ; APPLICANT: COHEN, CHARLES M.
 ; TITLE OF INVENTION: MORPHOGEN-INDUCED LIVER REGENERATION
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
 ; STREET: 45 SOUTH STREET
 ; CITY: HOPKINTON
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 01748

; COMPUTER READABLE FORM:
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/445,468A
 ; FILING DATE: 22-MAY-1995
 ; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:
 ; NAME: FENTON ESQ., GILLIAN M.
 ; REGISTRATION NUMBER: 36,508
 ; REFERENCE/DOCKET NUMBER: CRP-072FW2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 248-7560
 ; TELEFAX: (617) 248-7100
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 402 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-445-468A-21

Query Match 48.1%; Score 39; DB 2; Length 402;
 Best Local Similarity 58.3%; Pred. No. 1.9e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSP 12
 ||||:||||
 Db 235 LLGQAPRSQQP 246

RESULT 37
 US-08-901-200A-8
 ; Sequence 8, Application US/08901200A
 ; Patent No. 5854071
 ; GENERAL INFORMATION:

APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: OP3-INDUCED MORPHOGENESIS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/901,200A
FILING DATE: 28-JUL-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: CRP-076DV2
TELEPHONE: (508) 435-9001
TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-901-200A-8

Query Match 48.1%; Score 39; DB 2; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LIGNSPRTQSP 12
|||:|
Db 235 LIGQAPRSQP 246

RESULT 38
US-08-449-700-29
Sequence 29, Application US/08449700
Patent No. 5863758
GENERAL INFORMATION:
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/449,700
FILING DATE: 21-FEB-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: FITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-700-29

Query Match 48.1%; Score 39; DB 2; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LIGNSPRTQSP 12
|||:|
Db 235 LIGQAPRSQP 246

RESULT 39

```
US-08-449-699A-29
; Sequence 29, Application US/08449699A
; Patent No. 5958441
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: ANTIBODIES TO OSTEOGENIC PROTEINS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,699A
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/147,023
; FILING DATE: 01-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: STK-001CP6CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-449-699A-29

Query Match 48.1%; Score 39; DB 2; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSPRTQSP 12
|||:|:|
Db 235 LLGORAPRSQSP 246

RESULT 40
US-08-461-397A-21
; Sequence 21, Application US/08461397A
; Patent No. 5972884
; GENERAL INFORMATION:
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: CHARETTE, MARC F.
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: PANG, ROY H.L.
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: SMART, JOHN E.
; TITLE OF INVENTION: MORPHOGEN TREATMENT FOR LIMITING
; PROLIFERATION OF EPITHELIAL CELLS.
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,088
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,729
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER Esq., EDMUND R.
; REGISTRATION NUMBER: 27,829

US-08-449-699A-29
; Sequence 29, Application US/08449699A
; Patent No. 5958441
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,397A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER Esq., EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-074FW2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-397A-21

Query Match 48.1%; Score 39; DB 2; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSPRTQSP 12
|||:|:|
Db 235 LLGORAPRSQSP 246

RESULT 41
US-08-912-088-21
; Sequence 21, Application US/08912088
; Patent No. 5994131
; GENERAL INFORMATION:
; APPLICANT: SMART, JOHN
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,088
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,729
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER Esq., EDMUND R.
; REGISTRATION NUMBER: 27,829
```

REFERENCE/DOCKET NUMBER: CRP-058CPFW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-088-21

Query Match 48.1%; Score 39; DB 2; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLGNSPRTQSP 12
||| :||:|
Db 235 LLGQAPRSQQP 246

RESULT 42
US-08-278-730A-21
Sequence 21, Application US/08278730A
Patent No. 6022853
GENERAL INFORMATION:
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: COHEN, CHARLES M.
APPLICANT: RUEGER, DAVID C.
APPLICANT: OPPERMAN, HERMAN
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: MORPHOGENIC-ENRICHED DIETARY COMPOSITION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA USA
COUNTRY: USA
ZIP: 01748

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,730A
FILING DATE: 20-JULY-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: FENTON Esq., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-071FW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-278-730A-21

Query Match 48.1%; Score 39; DB 3; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLGNSPRTQSP 12
||| :||:|
Db 235 LLGQAPRSQQP 246

RESULT 43
US-08-889-419-6
Sequence 6, Application US/08889419
Patent No. 6071708
GENERAL INFORMATION:
APPLICANT: JONES, WILLIAM K
APPLICANT: TUCKER, RONALD F
APPLICANT: RUEGER, DAVID C
APPLICANT: OPPERMAN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
TITLE OF INVENTION: NOVEL MORPHOGENIC PROTEIN COMPOSITIONS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Administrator, Testa, Hurwitz &
ADDRESSEE: Thibeault, LLP
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,419
FILING DATE: 08-JUL-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,346
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: CRP-081DVCN

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-889-419-6

Query Match 48.1%; Score 39; DB 3; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLGNSPRTQSP 12
||| :||:|
Db 235 LLGQAPRSQQP 246

RESULT 44
US-08-445-467-21
Sequence 21, Application US/08445467
Patent No. 6077823
GENERAL INFORMATION:
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: PANG, ROY HL
APPLICANT: OPPERMAN, HERMANN
APPLICANT: RUEGER, DAVID C
APPLICANT: COHEN, CHARLES M
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: SMART, JOHN E
TITLE OF INVENTION: MORPHOGEN-INDUCED MODULATION OF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: CREATIVE BIOMOLECULES, INC.
STREET: 35 SOUTH STREET

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; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,467
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/165,511
; FILING DATE:
; APPLICATION NUMBER: US/07/938,336
; FILING DATE:
; APPLICATION NUMBER: US 07/667,274
; FILING DATE: 11-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/753,059
; FILING DATE: 30-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/752,764
; FILING DATE: 30-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-059CF.APP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-445-467-21

Query Match 48.1%; Score 39; DB 3; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSP 12
Db 235 LLGQAPRSQQP 246

RESULT 45
US-08-480-515A-21
; Sequence 21, Application US/08480515A
; Patent No. 6090776
; GENERAL INFORMATION:
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: PANG, ROY H.L.
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: SMART, JOHN E.
; TITLE OF INVENTION: MORPHOGEN TREATMENT OF ORGAN TRANSPLANTS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,467
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/901,200
; FILING DATE: 28-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, THOMAS C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: CRP-076DV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 435-9001
; TELEFAX: (508) 435-6951
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; MOLECULE TYPE: protein
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,515A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON ESQ., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-068FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7560
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-480-515A-21

Query Match 48.1%; Score 39; DB 3; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSP 12
Db 235 LLGQAPRSQQP 246

RESULT 46
US-09-219-391-8
; Sequence 8, Application US/09219391
; Patent No. 6153583
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: OP3-INDUCED MORPHOGENESIS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/219,391
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/901,200
; FILING DATE: 28-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, THOMAS C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: CRP-076DV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 435-9001
; TELEFAX: (508) 435-6951
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-219-391-8

Query Match      48.1%; Score 39; DB 3; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 LLGNSSPRQSP 12
      |||:|:|
Db      235 LLGQAPRSQQP 246

RESULT 47
US-09-170-936-21
; Sequence 21, Application US/09170936
; Patent No. 6333312
; GENERAL INFORMATION:
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; APPLICANT: SMART, JOHN E.
; TITLE OF INVENTION: TREATMENT TO PREVENT LOSS OF AND/OR
; TITLE OF INVENTION: INCREASE BONE MASS IN METABOLIC BONE DISEASES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/170,936
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/432,883
; FILING DATE: 2-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON Esq., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-060CPFWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7560
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-170-936-21

Query Match      48.1%; Score 39; DB 3; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 LLGNSSPRQSP 12
      |||:|:|
Db      235 LLGQAPRSQQP 246

RESULT 48
US-08-402-542-6

; Sequence 6, Application US/08402542
; Patent No. 6395883
; GENERAL INFORMATION:
; APPLICANT: JONES, WILLIAM K
; APPLICANT: TUCKER, RONALD F
; APPLICANT: RUEGER, DAVID C
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; TITLE OF INVENTION: NOVEL MORPHOGENIC PROTEIN COMPOSITIONS
; TITLE OF INVENTION: OF MATTER
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR/CREATIVE BIOMOLECULES,
; ADDRESS: INC.
; STREET: 35 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/402,542
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/040,510
; FILING DATE:
; APPLICATION NUMBER: US 08/029,335
; FILING DATE: 04-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/971,091
; FILING DATE: 03-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,235
; FILING DATE: 16-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,336
; FILING DATE: 08-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/923,780
; FILING DATE: 31-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-081CP
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-402-542-6

Query Match      48.1%; Score 39; DB 3; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 LLGNSSPRQSP 12
      |||:|:|
Db      235 LLGQAPRSQQP 246

RESULT 49
US-08-461-113-21
; Sequence 21, Application US/08461113
; Patent No. 6399569
; GENERAL INFORMATION:
; APPLICANT: COHEN, CHARLES M.
```

```

; APPLICANT: CHARETTE, MARC F.
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: PANG, ROY H.L.
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: SMART, JOHN E.
; TITLE OF INVENTION: MORPHOGEN TREATMENT FOR LIMITING
; TITLE OF INVENTION: PROLIFERATION OF EPITHELIAL CELLS.
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,113
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/445,882
; FILING DATE: 22-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON Esq., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-074DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 435-6951
; TELEFAX: (508) 435-6951
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-461-113-21

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Query Match 48.1%; Score 39; DB 3; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 LLGNSSPRTQSP 12
Db 235 LLQGRAPRSQQP 246

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RESULT 50
US-08-456-033-21
; Sequence 21, Application US/08456033
; Patent No. 6495513
; GENERAL INFORMATION:
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: PANG, ROY H.L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGEN-INDUCED NERVE REGENERATION AND
; TITLE OF INVENTION: REPAIR.
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA

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; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,033
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON Esq., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-070DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 435-9001
; TELEFAX: (508) 435-6951
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-456-033-21

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Query Match 48.1%; Score 39; DB 4; Length 402;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 LLGNSSPRTQSP 12
Db 235 LLQGRAPRSQQP 246

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Search completed: August 25, 2005, 11:45:23
Job time : 44 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2005, 11:34:33 ; Search time 40 Seconds
(without alignments)
36.081 Million cell updates/sec

Title: US-10-803-541-2

Perfect score: 81

Sequence: 1 LLGSSPRTPSPQNC 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR_79:*

1: Pirl:*

2: Pirl2:*

3: Pirl3:*

4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	664	1	VEHULA
2	73	90.1	665	2	S27267
3	69	85.2	665	2	S28182
4	44	54.3	521	2	F87775
5	44	54.3	970	2	S63059
6	42	51.9	291	2	E97463
7	42	51.9	690	2	S28222
8	42	51.9	2150	2	S71629
9	41	50.6	148	2	AH2488
10	41	50.6	439	2	A12098
11	41	50.6	542	1	T02074
12	41	50.6	542	2	T03789
13	41	50.6	599	2	I53395
14	41	50.6	717	2	S31034
15	41	50.6	717	2	S31035
16	41	50.6	2038	2	A43742
17	40.5	50.0	470	2	S71466
18	40	49.4	94	2	E82515
19	40	49.4	199	2	S56155
20	40	49.4	212	2	H90369
21	40	49.4	454	2	I51916
22	40	49.4	551	2	A12964
23	40	49.4	690	2	D98318
24	40	49.4	1017	2	A37227
25	40	49.4	1020	2	A34474
26	40	49.4	1020	2	B24639
27	40	49.4	1031	2	I51674
28	40	49.4	1033	2	I49143
29	40	49.4	1033	2	A25344

30	40	49.4	1034	2	JN0903	H+/K+-exchanging A
31	40	49.4	1034	2	A31671	H+/K+-exchanging A
32	40	49.4	1035	2	A35292	H+/K+-exchanging A
33	40	49.4	1035	2	S23406	H+/K+-exchanging A
34	39	48.1	169	2	S20484	osreogenic prote
35	39	48.1	402	2	A45056	envelope surface g
36	39	48.1	403	2	B46165	hypothetical prote
37	39	48.1	408	2	C46165	hypothetical prote
38	39	48.1	481	2	T16484	CED-6 protein - Ca
39	39	48.1	492	2	T43064	coat protein gamma
40	39	48.1	563	2	S33957	env polypeptide pr
41	39	48.1	642	1	VCWVS2	env polypeptide pr
42	39	48.1	642	2	T10533	env polypeptide pr
43	39	48.1	645	1	VCWVS3	lamin - chicken
44	39	48.1	657	1	S05517	env polypeptide -
45	39	48.1	662	1	VCWVGF	env polypeptide -
46	39	48.1	662	2	A25982	transcription regu
47	39	48.1	727	2	B60191	filensin - bovine
48	39	48.1	755	2	S32103	EVI1 protein - hum
49	39	48.1	1042	2	S41705	transcription regu
50	39	48.1	1042	2	A31591	oncogene Evi-1 - h
51	39	48.1	1051	2	A60191	nicotinic acetylch
52	38.5	47.5	470	2	A39218	KIAA1424 protein [
53	38.5	47.5	1944	2	A59438	ALR protein - huma
54	38.5	47.5	5262	2	T03454	hypothetical prote
55	38	46.9	81	2	AH2564	Na+/K+-exchanging
56	38	46.9	220	2	S20970	probable transcrip
57	38	46.9	227	2	D83543	hypothetical prote
58	38	46.9	278	2	F85012	conserved hypotet
59	38	46.9	289	2	T42994	hypothetical prote
60	38	46.9	290	2	T44550	conserved hypotet
61	38	46.9	292	2	T40045	hypothetical prote
62	38	46.9	305	2	T45062	hypothetical prote
63	38	46.9	353	2	S22805	env polypeptide -
64	38	46.9	381	2	T10707	adenosylmethionine
65	38	46.9	445	1	VCFMVL	env polypeptide -
66	38	46.9	522	2	E84833	hypothetical prote
67	38	46.9	534	1	VCWVSF	env polypeptide -
68	38	46.9	575	2	T01552	hypothetical prote
69	38	46.9	627	1	VCVMW2	env polypeptide -
70	38	46.9	630	2	A39344	tumor-associated m
71	38	46.9	631	2	I52257	episialin - mouse
72	38	46.9	636	1	VCWVFS	env polypeptide pr
73	38	46.9	639	1	VCWVSA	env polypeptide -
74	38	46.9	640	1	VCVMW1	env polypeptide pr
75	38	46.9	640	1	VCVMRV	gp70 protein - mur
76	38	46.9	644	2	S15464	env polypeptide -
77	38	46.9	662	1	VCMWLB	env polypeptide pr
78	38	46.9	665	1	VCMWKA	env polypeptide pr
79	38	46.9	665	1	VCWVVR	env polypeptide -
80	38	46.9	665	1	VCWVEM	env polypeptide pr
81	38	46.9	668	1	VCMVFP	env polypeptide -
82	38	46.9	669	1	VCWVEK	envelope protein -
83	38	46.9	669	2	A46511	env polypeptide pr
84	38	46.9	676	1	T01381	env protein - muri
85	38	46.9	676	2	S70395	env polypeptide -
86	38	46.9	688	2	A43491	env polypeptide -
87	38	46.9	688	2	A43491	env polypeptide -
88	38	46.9	689	2	B43491	env polypeptide -
89	38	46.9	781	2	A26641	Na+/K+-exchanging
90	38	46.9	821	2	S26708	hypothetical prote
91	38	46.9	899	2	F83391	protein R06B10.4 [
92	38	46.9	1010	2	B37227	Na+/K+-exchanging
93	38	46.9	1013	1	S00801	Na+/K+-exchanging
94	38	46.9	1013	2	C24639	Na+/K+-exchanging
95	38	46.9	1021	1	PWSHNA	Na+/K+-exchanging
96	38	46.9	1021	1	S04630	Na+/K+-exchanging
97	38	46.9	1021	2	A28199	Na+/K+-exchanging
98	38	46.9	1021	2	B24862	Na+/K+-exchanging
99	38	46.9	1022	2	S49127	Na+/K+-exchanging
100	38	46.9	1023	1	A24639	Na+/K+-exchanging

ALIGNMENTS

```

RESULT 1
VEHULA
lamin A - human
N:Alternate names: 70kDa lamin
C:Species: Homo sapiens (man)
C>Date: 28-May-1986 #sequence revision 04-Dec-1986 #text_change 09-Jul-2004
C:Accession: A02961; B24249; C24249
R:McKeon, F.D.; Kirschner, M.W.; Caput, D.
Nature 319, 463-468, 1986
A:Title: Homologies in both primary and secondary structure between nuclear envelope and
A:Reference number: A02962; MUID:86118697; PMID:3453101
A:Accession: A02961
A:Molecule type: mRNA
A:Residues: 1-582, 'LAHRAVRDLRAACRQICQLRSPGGRTHL', 'LWLFCLQCHGHSQLPQCGQGWQLRGQSG', 'HPH
A:Cross-references: UNIPROT:P02545; GB:X03444; NID:g34227; PIDN:CAA27173.1; PID:g34228
A:Note: this sequence has been corrected in reference A94121; an omitted nucleotide cause
R:Fisher, D.Z.; Chaudhary, N.; Blobel, G.
Proc. Natl. Acad. Sci. U.S.A. 83, 6450-6454, 1986
A:Title: cDNA sequencing of nuclear lamins A and C reveals primary and secondary structu
A:Reference number: A94121; MUID:86313596; PMID:3462705
A:Note: parts of sequences from rat lamins, but not human, were determined by protein se
A:Accession: B24249
A:Molecule type: mRNA
A:Residues: 537-664 <PIS>
A:Note: sequence fragment shown in publication
A:Accession: C24249
A:Molecule type: mRNA
A:Residues: 150-664 <PI2>
A:Cross-references: GB:M13452; NID:g186838; PIDN:AAA36160.1; PID:g386856
A:Note: submitted sequence extracted from GenBank
C:Comment: The lamins A and C (see CIR:VEHULC) are products of alternative splicing of the s
C:Comment: The lamins (A, B, and C) contains several alpha-helical domains capable of fo
C:Comment: The association of lamins, dependent upon ionic interactions, is interrupted
rates with lamin' dissociation; it does not reform until telophase, when the lamins are d
C:Genetics8;
A:Gene: GDB:LMNA; LMNI
A:Cross-references: GDB:132146; OMIM:150330
A:Map position: lq21.2-lq21.3
C:Function:
C:Description: structural component of the nuclear lamina, a fibrous meshwork on the nuc
C:Superfamily: cytoskeletal keratin
C:Keywords: alternative splicing; coiled coil; lipoprotein; membrane protein; methylated
F:2-661/Product: lamin A #status predicted <NAT>
F:2-33/Domain: head <HED>
F:34-388/Domain: rod <ROD>
F:34-70/Region: coil 1A
F:81-218/Region: coil 1B
F:243-388/Region: coil 2
F:325/Region: stutter
F:389-661/Domain: tail <END>
F:417-420/Region: nuclear location signal
F:661/Binding site: farnesyl (Cys) (covalent) #status predicted
F:661/Modified site: methyl ester carboxyl end (Cys) (in mature form) #status predicted

Query Match 100.0%; Score 81; DB 1; Length 664;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLGNSSPRTQSPQNC 15
DB 647 LLGNSSPRTQSPQNC 661

RESULT 2
S27267
lamin A - rat
N:Contains: nucleoside-triphosphatase (EC 3.6.1.15)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 22-Nov-1993 #sequence revision 27-Jan-1995 #text_change 10-Dec-1999
C:Accession: S27267; S30573; A60832; S41934

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R:Ozaki, T.; Sakiyama, S.
FEBS Lett. 312, 165-168, 1992
A:Title: Lamin A gene expression is specifically suppressed in v-src-transformed cells.
A:Reference number: S27267; MUID:93050186; PMID:1426247
A:Accession: S27267
A:Molecule type: mRNA
A:Residues: 1-665 <OZA>
A:Cross-references: GB:X66870; NID:g56550; PIDN:CAA47342.1; PID:g56551
A:Note: the authors translated the codon CAG for residue 258 as Glu
A:Note: the nucleotide sequence in GB:X66870 (see reference S30573) differs from the pub:
R:Ozaki, T.; Sakiyama, S.
submitted to the EMBL Data Library, May 1992
A:Reference number: S30573
A:Accession: S30573
A>Status: significant sequence differences
A:Molecule type: mRNA
A:Cross-references: GB:X66870; NID:g56550; PID:g56551
A:Note: the nucleotide sequence in GB:X66870 differs from the published version (see ref:
R:Clawson, G.A.; Lackey, A.; Tokes, Z.A.
Exp. Cell Res. 176, 180-186, 1988
A:Title: The 46-kDa nucleoside triphosphatase of rat liver nuclear scaffold represents th
A:Reference number: A60832; MUID:88225292; PMID:2836227
A:Accession: A60832
A:Molecule type: protein
A:Residues: 12-25;29-33, 'L',35-40,'K',42;198-202,'Q',204-209;282-296;352-366 <CLA>
R:Jonnalagadda, V.S.; Parmaik, V.K.
submitted to the EMBL Data Library, November 1993
A:Reference number: S41934
A:Accession: S41934
A:Molecule type: mRNA
A:Residues: 26-82,'A',84-469,'K',471-523,'T',525-583,'R',585,'R',587-605,'A',607-665 <JON
A:Cross-references: EMBL:X76297; NID:g453179; PIDN:CAA53945.1; PID:g453180
C:Superfamily: cytoskeletal keratin
C:Keywords: blocked amino end; coiled coil; hydrolase; nuclear membrane; phosphoprotein
F:1-390/Domain: head #status predicted <HEA>
F:31-390/Domain: rod #status predicted <ROD>
F:391-665/Domain: tail #status predicted <TAI>
F:22,392,404,406/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 90.1%; Score 73; DB 2; Length 665;
Best Local Similarity 93.3%; Pred. No. 0.00028;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLGNSSPRTQSPQNC 15
DB 648 LLGNSSPRTQSPQNC 662

RESULT 3
S28182
lamin A - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Nov-1993 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S28182; S06662; S65931
R:Nakajima, N.; Sado, T.
Biochim. Biophys. Acta 1171, 311-314, 1993
A:Title: Nucleotide sequence of a mouse lamin A cDNA and its deduced amino acid sequence
A:Reference number: S28182; MUID:93144345; PMID:7916626
A:Accession: S28182
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-665 <NAK>
A:Cross-references: UNIPROT:Q91WF2; UNIPROT:Q9DC21
R:Weber, K.; Flessmann, U.; Traub, P.
FEBS Lett. 257, 411-414, 1989
A:Title: Maturation of nuclear lamin A involves a specific carboxy-terminal trimming, whi
a.
A:Reference number: S06662; MUID:90060368; PMID:2583287
A:Accession: S06662
A:Molecule type: protein
A:Residues: 520-580,'X',582-622,'V',624-647 <WEB>
R:Nakajima, N.; Abe, K.
FEBS Lett. 365, 108-114, 1995

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A;Title: Genomic structure of the mouse A-type lamin gene locus encoding somatic and germline proteins
A;Reference number: S65931; MUID:95300954; PMID:7781761
A;Accession: S65931
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-117 <NAW>
A;Cross-references: EMBL:D49732; NID:gl100724
A;Superfamily: cytoskeletal keratin
C;Keywords: alternative splicing; coiled coil; intermediate filament; lipoprotein; nucleoside triphosphatase
F;1-33/Domain: head #status predicted <ROD>
F;34-388/Domain: rod #status predicted <ROD>
F;34-218/Region: coiled coil 1
F;243-388/Region: coiled coil 2
F;266/Region: heptad change of phase
F;325/Region: stutter
F;330/Region: heptad change of phase
F;389-662/Domain: tail #status predicted <END>
F;417-420/Region: nuclear location signal
P;662/Binding site: farneesyl (Cys) (covalent) #status predicted

Query Match 85.2%; Score 69; DB 2; Length 665;
Best Local Similarity 86.7%; Pred. No. 0.0013;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLGNSPRTQSPQC 15
Db 648 LLGNSPRTQSPQC 662

RESULT 4
P87775
Protein C24A11.8 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: F87775
R;anonymouse, The C. elegans Sequencing Consortium.
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
A;Reference number: AF5000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 282, 2012-2018, 1998
A;Accession: F87775
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-521 <STO>
A;Cross-references: GB:chr_I; PIDN:AAB37677.1; PID:gl703630; GSPDB:GN00019; CESP:C24A11.8
A;Gene: C24A11.8
A;Map position: 1

Query Match 54.3%; Score 44; DB 2; Length 521;
Best Local Similarity 61.5%; Pred. No. 16;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSPRTQSPQ 13
Db 40 IIGNEFPRTQSAQ 52

RESULT 5
S63059
hypothetical protein YNL118c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N1917
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 16-Aug-2004
C;Accession: S63059; S59701; S67340
R;De Antoni, A.; D'Angelo, M.; Dal Pero, F.; Sartorello, F.; Pandolfo, D.; Lanfranchi, G.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63047
A;Accession: S63059
A;Molecule type: DNA
A;Residues: 1-970 <DEA>
A;Cross-references: UNIPROT:P53550; EMBL:Z71394; NID:gl302044; PID:e239800; PID:gl302045

A;Experimental source: strain S288C
R;Tzagoloff, A.A.
submitted to the EMBL Data Library, June 1995
A;Description: Suppressor of a yeast pet mutant.
A;Reference number: S59701
A;Accession: S59701
A;Molecule type: DNA
A;Residues: 1-424, 'L', 426-970 <TZA>
A;Cross-references: EMBL:L43065; NID:9870733; PID:9870734
A;Experimental source: strain D273-10B
R;d'Antoni, A.; d'Angelo, M.; dal Pero, F.; Sartorello, F.; Pandolfo, D.; Lanfranchi, G.
submitted to the EMBL Data Library, February 1996
A;Description: The DNA sequence of cosmid 14-13b from chromosome XIV of Saccharomyces cerevisiae
A;Reference number: S67327
A;Accession: S67340
A;Molecule type: DNA
A;Residues: 1-970 <DAN>
A;Cross-references: EMBL:Z69382; NID:gl183941; PID:e221828; PID:gl183955
C;Genetics:
A;Map position: 14L
C;Superfamily: mut domain homology
F;129-163/Domain: mut domain homology <MUT>

Query Match 54.3%; Score 44; DB 2; Length 970;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GNSPRTQSPON 14
Db 595 GKSPSTQSKQN 606

RESULT 6
E97463
1564 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: E97463
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: E97463
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-291 <KUR>
A;Cross-references: UNIPROT:Q8UH30; GB:AE007869; PIDN:AAK86662.1; PID:gl5155844; GSPDB:G
C;Genetics:
A;Gene: AGR_C1564
A;Map position: circular chromosome

Query Match 51.9%; Score 42; DB 2; Length 291;
Best Local Similarity 58.3%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LGNSPRTQSPQ 13
Db 18 LSHTTPRTQSPQ 29

RESULT 7
S28222
peroxidase (EC 1.11.1.7) precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S28222; S25522
R;Ng, S.W.; Wiedemann, M.; Kontermann, R.; Petersen, G.
Biochim. Biophys. Acta 1171, 224-228, 1992
A;Title: Molecular characterization of a putative peroxidase gene of Drosophila melanogaster
A;Reference number: S28222; MUID:93129626; PMID:1482687

```
A;Accession: S28222
A;Molecule type: DNA
A;Residues: 1-690 <NS>
A;Cross-references: UNIPROT:Q01603; EMBL:X68131; NID:G2511639; PIDN:CAA48238.1; PID:G833
C;Genetics:
A;Gene: FlyBase:Pxd
A;Cross-references: FlyBase:FBgn0004577
A;Introns: 57/2; 126/2; 197/1; 445/2; 497/3; 621/1; 656/2
C;Superfamily: myeloperoxidase; myeloperoxidase homology
C;Keywords: glycoprotein; oxidoreductase
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-690/Product: myeloperoxidase #status predicted <NAT>
F;310/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.9%; Score 42; DB 2; Length 690;
Best Local Similarity 50.0%; Pred. No. 45;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSPQN 14
::|||:::|
Db 55 VIGNSLPSPAPQN 68

RESULT 8
S71629
sensory transduction histidine kinase dhka - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C;Accession: S71629
R;Wang, N.; Shauleky, G.; Escalante, R.; Loomis, W.F.
EMBO J. 15, 3890-3898, 1996
A;Title: A two-component histidine kinase gene that functions in Dictyostelium developme
A;Reference number: S71629; MUID:96324397; PMID:8670894
A;Accession: S71629
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-2150 <NAN>
A;Cross-references: UNIPROT:Q23863; EMBL:U42597
A;Experimental source: strain Ax4
C;Genetics:
A;Gene: dhka
A;Map position: 6
C;Keywords: autophosphorylation; phosphoprotein; phosphotransferase; two-component regul
F;2076/Binding site: phosphate (Asp) (covalent) #status predicted

Query Match 51.9%; Score 42; DB 2; Length 2150;
Best Local Similarity 53.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GNSSPRTQSPQNC 15
|||:::|
Db 345 GNNSPRSCGSGNC 357

RESULT 9
AH2488
hypothetical protein alr7088 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120al
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AH2488
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpō, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2488
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-148 <KUR>
A;Cross-references: UNIPROT:Q8YL47; GB:BA000020; PIDN:BA078172.1; PID:G17135626; GSPDB:G
A;Experimental source: strain PCC 7120
```

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C;Genetics:
A;Gene: alr7088
A;Genome: plasmid

Query Match 50.6%; Score 41; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TQSPQNC 15
|||||
Db 85 TQSPQNC 91

RESULT 10
AI2098
hypothetical protein all2344 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AI2098
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpō, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AI2098
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-439 <KUR>
A;Cross-references: UNIPROT:Q8YUK2; GB:BA000019; PIDN:BA074043.1; PID:G17131436; GSPDB:G
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all2344

Query Match 50.6%; Score 41; DB 2; Length 439;
Best Local Similarity 70.0%; Pred. No. 42;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GNSSPRTQSP 12
|||||:::
Db 257 GNSSPTTNP 266

RESULT 11
T02074
4-coumarate-CoA ligase (EC 6.2.1.12) - common tobacco
N;Alternate names: 4-coumaroyl-CoA synthetase
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: T02074
R;Katayama, Y.; Kawai, S.; Morohoshi, N.; Kajita, S.
submitted to the EMBL Data Library, December 1994
A;Description: Cloning and nucleotide sequence of 4-coumarate:coenzyme A ligase gene from
A;Reference number: Z14545
A;Accession: T02074
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-542 <NAT>
A;Cross-references: UNIPROT:Q42943; EMBL:DA3773; PIDN:BA007828.1
C;Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology
C;Keywords: acid-thiol ligase; coenzyme A; flavonoid biosynthesis
F;73-532/Domain: acetate-CoA ligase homology <ACL>

Query Match 50.6%; Score 41; DB 1; Length 542;
Best Local Similarity 61.5%; Pred. No. 52;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GNSSPRTQSPQNC 15
|||||:::
Db 377 GNSLPNQSGEIC 389

RESULT 12
```


F;1-1106/Product: female sterile homeotic protein, 110K #status predicted <MAT>
 F;59-1116/Domain: bromodomain homology <BRO1>
 F;503-560/Domain: bromodomain homology <BRO2>

Query Match 50.6%; Score 41; DB 2; Length 2038;
 Best Local Similarity 66.7%; Pred. No. 1.9e+02;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 LLGNSPRTQSPQN 14
 ||||| |||||
 Db 1985 QQSSPAQQSPQD 1996

RESULT 17

homeotic protein SOX-12 protein - African clawed frog
 N/Alternate names: SRY-related protein
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 16-Aug-2004
 C/Accession: S71466; S22947; S21490
 R/Komatsu, N.; Hiraoka, Y.; Shiozawa, M.; Ogawa, M.; Aiso, S.
 Biochim. Biophys. Acta 1305, 117-119, 1996
 A/Title: Cloning and expression of Xenopus laevis xSox12 cDNA.
 A/Reference number: S71466; MUID:96180312; PMID:8597594
 A/Accession: S71466
 A/Molecule type: mRNA
 A/Residues: 1-470 <KOW>
 A/Cross-references: UNIPROT:P40649; EMBL:D50552; NID:gi255903; PIDN:BA09119.1; PID:d100
 A/Experimental source: ovary
 R/Denny, P.; Swift, S.; Brand, N.; Dabhadre, N.; Barton, P.; Ashworth, A.
 Nucleic Acids Res. 20, 2887, 1992
 A/Title: A conserved family of genes related to the testis determining gene, SRY.
 A/Reference number: S22935; MUID:92310993; PMID:1614875
 A/Accession: S22947
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 308-359 <DEN>
 A/Cross-references: EMBL:X65655; NID:g65261; PIDN:CAA46606.1; PID:g938305
 C/Genetics:
 C/Superfamily: HMG box homology
 C/Keywords: DNA binding; leucine zipper
 F;35-54/Region: leucine zipper
 F;294-367/Domain: HMG box homology <HMG1>

Query Match 50.0%; Score 40.5; DB 2; Length 470;
 Best Local Similarity 66.7%; Pred. No. 55;
 Matches 10; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

Qy 1 LLGNSPRTQSPQNC 15
 ||||| |||||
 Db 415 LLGNLS---QSPQEC 426

RESULT 18

hypothetical protein XF2717 [imported] - Xylella fastidiosa (strain 9a5c)
 C/Species: Xylella fastidiosa
 C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C/Accession: E82515
 R/Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
 Nature 406, 151-157, 2000
 A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A/Reference number: E82515; MUID:20365717; PMID:10910347
 A/Note: for a complete list of authors see reference number A59328 below
 A/Accession: E82515
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-94 <SIM>
 A/Cross-references: UNIPROT:Q9PA03; GB:AE004078; GB:AE003849; NID:g9187832; PIDN:AAF8579
 A/Experimental source: strain 9a5c
 R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir, H.

as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
 A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, B.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A/Reference number: A59328
 A/Contents: annotation
 C/Genetics:
 A/Gene: XF2717

Query Match 49.4%; Score 40; DB 2; Length 94;
 Best Local Similarity 42.9%; Pred. No. 13;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSPRTQSPQN 14
 :|||: |||||
 Db 5 VIGNHTPTTSPES 18

RESULT 19

S56155
 sulfocyanin - Sulfolobus acidocaldarius
 N/Alternate names: blue copper protein
 C/Species: Sulfolobus acidocaldarius
 C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
 C/Accession: S56155
 R/Castresana, J.; Luebben, M.; Saraste, M.
 J. Mol. Biol. 250, 202-210, 1995
 A/Title: New archaeobacterial genes coding for redox proteins: implications for the evolu
 A/Reference number: S56155; MUID:95333177; PMID:7608970
 A/Accession: S56155
 A/Status: preliminary; nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-199 <CAS>
 A/Cross-references: UNIPROT:Q53765; EMBL:Z48338; NID:g927521; PID:g927523
 F;7-34/Domain: transmembrane #status predicted <TRM>
 F;110,171,176,181/Binding site: copper (His, Cys, His, Met) (type 1) #status predicted

Query Match 49.4%; Score 40; DB 2; Length 199;
 Best Local Similarity 61.5%; Pred. No. 28;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSPRTQSPQ 13
 ||||| |||||
 Db 114 LLNSTPTQSPPE 126

RESULT 20

H90369
 2-haloalkanoic acid dehalogenase [imported] - Sulfolobus solfataricus
 C/Species: Sulfolobus solfataricus
 C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C/Accession: H90369
 R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
 arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
 submitted to GenBank, April 2001
 A/Description: Sulfolobus solfataricus complete genome.
 A/Reference number: A99139
 A/Accession: H90369
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-212 <KUR>
 A/Cross-references: UNIPROT:Q97WT6; GB:AE006641; NID:gl3815309; PIDN:AAK42215.1; GSPDB:G

Query Match 49.4%; Score 40; DB 2; Length 212;
 A/Gene: SSO2028

Best Local Similarity 80.0%; Pred. No. 30;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLGNSSPRTQ 10
DB 110 LLGNSSPRTK 119

RESULT 21
I51916
H+/K+-exchanging ATPase (EC 3.6.3.10) alpha chain - rat (fragment)
C:Species: Rattus sp. (rat)
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 19-Apr-2002
A:Accession: I51916
R:Ahn, K.Y.; Kone, B.C.
Am. J. Physiol. 268, F99-F109, 1995
A:Title: Expression and cellular localization of mRNA encoding the 'gastric' isoform of
A:Reference number: I51916; MUID:95142238; PMID:7840253
A:Accession: I51916
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-454 <RES>
A:CROSS-references: GB:S74801; NID:g802079
A:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: ATP; hydrolase; phosphoprotein
F:332/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 49.4%; Score 40; DB 2; Length 454;
Best Local Similarity 53.8%; Pred. No. 64;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLGNSSPRTQSPQ 13
DB 174 LTGESEPQTRSPQ 186

RESULT 22
A12964
Hypothetical protein Atu322 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
A:Accession: A12964
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
i Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: A12964
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-551 <KUR>
A:CROSS-references: UNIPROT:Q8UAQ1; GB:AE008689; PIDN:AAL44135.1; PID:g17741707; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu322
A:Map position: linear chromosome

Query Match 49.4%; Score 40; DB 2; Length 551;
Best Local Similarity 61.5%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLGNSSPRTQSPQ 13
DB 536 LSGNGRPAQSPQ 548

RESULT 23
D98318
ABC protein AGR_L 3000 (AB015053) [imported] - Agrobacterium tumefaciens (strain C58, Ce
C:Species: Agrobacterium tumefaciens

C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: D98318
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: D98318
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-690 <KUR>
A:CROSS-references: UNIPROT:Q8UAQ1; GB:AE007870; PIDN:AAK90070.1; PID:g15160053; GSPDB:G
C:Genetics:
A:Gene: AGR_L 3000
A:Map position: linear chromosome

Query Match 49.4%; Score 40; DB 2; Length 690;
Best Local Similarity 61.5%; Pred. No. 97;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLGNSSPRTQSPQ 13
DB 675 LSGNGRPAQSPQ 687

RESULT 24
A37227
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-2 chain - chicken
C:Species: Gallus gallus (chicken)
C>Date: 16-Sep-1992 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
A:Accession: I50394; A37227
R:Takeyasu, K.; Lemas, M.; Fambrough, D.M.
Am. J. Physiol. 259, 619-630, 1991
A:Title: Stability of the Na+, K+-ATPase alpha-subunit isoforms in evolution.
A:Reference number: I50394
A:Accession: I50394
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1017 <TAK>
A:CROSS-references: UNIPROT:P24797; GB:M59599; NID:g212405; PIDN:AAA48981.1; PID:g212406
R:Takeyasu, K.; Lemas, V.; Fambrough, D.M.
Am. J. Physiol. 259, C619-C630, 1990
A:Title: Stability of Na(+)-K(+)-ATPase alpha-subunit isoforms in evolution.
A:Reference number: A37227; MUID:91023019; PMID:2171348
A:Accession: A37227
A:Molecule type: mRNA
A:Residues: 3-1017 <TA2>
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: ATP; glycoprotein; hydrolase; phosphoprotein
F:581-777/Domain: ATPase nucleotide-binding domain homology <ATN>
F:210,478/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:377/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 49.4%; Score 40; DB 2; Length 1017;
Best Local Similarity 53.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLGNSSPRTQSPQ 13
DB 213 LTGESEPQTRSPQ 225

RESULT 25
A34474
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-2 chain - human
N:Alternate names: Na+/K+-exchanging ATPase alpha chain-4; sodium/potassium transporting
C:Species: Homo sapiens (man)
C>Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004
A:Accession: A34474; B27795; D27397
R:Shull, M.M.; Pugh, D.G.; Lingrel, J.B.
J. Biol. Chem. 264, 17532-17543, 1989
A:Title: Characterization of the human Na,K-ATPase alpha2 gene and identification of int
A:Reference number: A34474; MUID:90008924; PMID:2477373

A>Title: Molecular cloning and structural analysis of canine gastric H⁺, K⁺-ATPase.
A/Reference number: JN0903; MUID:94071880; PMID:8250881
A/Accession: JN0903
A/Molecule type: mRNA
A/Residues: 1-1034 <SON>
A/Experimental source: stomach
A/Note: The authors translated the codon CGG for residue 728 as nothing
A/Note: the DNA sequence is also determined and has 21 introns
C/Comment: This enzyme functions as a proton pump in the secretion of hydrochloric acid
C/Genetics:
A/Introns: 4/3; 51/3; 71/3; 139/3; 177/3; 262/1; 351/3; 418/1; 454/3; 499/3; 564/1; 623/
C/Superfamily: Na/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C/Keywords: ATP; glycoprotein; hydrolase; ion transport; phosphoprotein; potassium trans;
F/597-793/Domain: ATPase nucleotide-binding domain homology <ATN>
F/225,493/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/386/Active site: Asp (aspartylphosphate intermediate) #status predicted
F/518/Binding site: ATP (Lys) #status predicted

Query Match 49.4%; Score 40; DB 2; Length 1034;
Best Local Similarity 53.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Df 228 LTGESEPTRSPE 240

QY 1 LLGNSSPRQTSPQ 13
| | | | | :
| | | | | :

Db 228 LTGESEPTRSPE 240

RESULT 31

A31671
H+/K+-exchanging ATPase (EC 3.6.3.10) alpha chain - pig
N/Alternate names: H+/K+-transporting ATPase
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-May-1990 #sequence revision 21-May-1990 #text_change 09-Jul-2004
C/Accession: A31671; A24228; S21269; S18375
R/Maeda, M.; Ishizaki, J.; Futai, M.
Biochem. Biophys. Res. Commun. 157, 203-209, 1988
A/Title: cDNA cloning and sequence determination of pig gastric (H⁺) + K(+))-ATPase.
A/Reference number: A31671; MUID:89061712; PMID:2848518
A/Accession: A31671
A/Molecule type: mRNA
A/Residues: 1-1034 <MAE>
A/Cross-references: UNIPROT:P19156; GB:M22724; NID:G164383; PIDN:AAA31003.1; PID:G164384
R/Lane, L.K.; Kirley, T.L.; Ball Jr., W.J
Biochem. Biophys. Res. Commun. 138, 185-192, 1986
A/Reference number: A24228; MUID:86295667; PMID:3017315
A/Accession: A24228
A/Molecule type: protein
A/Residues: 'Y', 3-18 <LAN>
R/Callaghan, J.M.; Tob, B.H.; Simpson, R.J.; Baldwin, G.S.; Gleeson, P.A.
Biochem. J. 283, 63-68, 1992
A/Title: Rapid purification of the gastric H(+)/K(+)-ATPase complex by tomato-lectin aff
A/Reference number: S21269; MUID:92231849; PMID:1314570
A/Accession: S21269
A/Molecule type: protein
A/Residues: 173-182; 777-783; 1022-1033 <CAL>
R/van Uem, T.J.F.; Swarts, H.G.P.; de Pont, J.J.H.H.M.
Biochem. J. 280, 243-248, 1991
A/Title: Determination of the epitope for the inhibitory monoclonal antibody 5-B6 on the
A/Reference number: S18375; MUID:92074982; PMID:1720615
A/Accession: S18375
A/Molecule type: protein
A/Residues: 'X', 49-53; 'X', 55-58; 'X', 380; 'X', 382-383; 'XX', 386; 'X', 457-458; 'X', 460-461 <VA
C/Superfamily: Na/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C/Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; potassium transport; transmem
F/597-793/Domain: ATPase nucleotide-binding domain homology <ATN>
F/225,493/Binding site: carbohydurate (Asn) (covalent) #status predicted
F/386/Active site: Asp (aspartylphosphate intermediate) #status experimental
F/518/Binding site: ATP (Lys) #status predicted

Query Match 49.4%; Score 40; DB 2; Length 1034;
Best Local Similarity 53.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Qy      1  LLGNSSPRTQSPQ 13
      |||  |||  |||  |||  |||
Db      228  LTGESEPTQTSPE 240

RESULT 32
A35292
H+/K+-exchanging ATPase (EC 3.6.3.10) alpha chain - human
N/Alternate names: H+/K+-transporting ATPase alpha chain
C/Species: Homo sapiens (man)
C/Date: 17-Aug-1990 #sequence_revision 06-Nov-1992 #text_change 09-Jul-2004
C/Accession: A36558; A35292
R/Newman, P.R.; Greeb, J.; Keeton, T.P.; Reyes, A.A.; Shull, G.E.
DNA Cell Biol. 9, 749-762, 1990
A/Title: Structure of the human gastric H,K-ATPase gene and comparison of the 5'-flankin
A/Reference number: A36558; MUID:91090845; PMID:2176086
A/Accession: A36558
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1035 <NEW>
A/Cross-references: UNIPROT:P20648; GB:M63962; NID:gl84106; PIDN:AAA35988.1; PID:gl84107
F/Maeda, M.; Oshiman, K.I.; Tamura, S.; Futai, M.
J. Biol. Chem. 265, 9027-9032, 1990
A/Title: Human Gastric H(+) + K(+) -ATPase gene. Similarity to (Na(+)+K(+))-ATPase gen
A/Reference number: A35292; MUID:90264383; PMID:2160952
A/Accession: A35292
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1035 <MAE>
A/Cross-references: GB:J05451; NID:g561633; PIDN:AAA51010.1; PID:g561634; GB:J05452
C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C/Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; transmembrane protein
F/598-794/Domain: ATPase nucleotide-binding domain homology <ATN>
F/226,494/Binding site: carbohydurate (Asn) (covalent) #status predicted
F/387/Active site: Asp (aspartylphosphate intermediate) #status predicted
F/519/Binding site: ATP (Lys) #status predicted

Query Match      49.4%; Score 40; DB 2; Length 1035;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches      7; Conservative      3; Mismatches      3; Indels      0; Gaps      0;

Qy      1  LLGNSSPRTQSPQ 13
      |||  |||  |||  |||  |||
Db      229  LTGESEPTQTSPE 241

RESULT 33
S23406
H+/K+-exchanging ATPase (EC 3.6.3.10) alpha chain - rabbit
N/Alternate names: H+/K+-transporting ATPase alpha chain
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C/Accession: S23406
R/Bamberg, K.; Mercier, F.; Reuben, M.A.; Kobayashi, Y.; Munson, K.B.; Sachs, G.
Biochim. Biophys. Acta 1131, 69-77, 1992
A/Title: cDNA cloning and membrane topology of the rabbit gastric H(+)/K(+)-ATPase alpha
A/Reference number: S23406; MUID:92256493; PMID:1316171
A/Accession: S23406
A/Molecule type: mRNA
A/Residues: 1-1035 <BAM>
A/Cross-references: UNIPROT:P27112; EMBL:X64694; NID:g1470; PIDN:CAA45927.1; PID:g1471
C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C/Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; transmembrane protein
F/598-794/Domain: ATPase nucleotide-binding domain homology <ATN>
F/226,494/Binding site: carbohydurate (Asn) (covalent) #status predicted
F/387/Active site: Asp (aspartylphosphate intermediate) #status predicted
F/519/Binding site: ATP (Lys) #status predicted

Query Match      49.4%; Score 40; DB 2; Length 1035;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches      7; Conservative      3; Mismatches      3; Indels      0; Gaps      0;

Qy      1  LLGNSSPRTQSPQ 13

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Db      229  LTGESEPTQTSPE 241
      |||  |||  |||  |||  |||

RESULT 34
S20484
hypothetical protein 2 - Azospirillum brasilense
C/Species: Azospirillum brasilense
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S20484
R/Vieille, C.; Elmerich, C.
Mol. Gen. Genet. 231, 375-384, 1992
A/Title: Characterization of an Azospirillum brasilense Sp7 gene homologous to Alcaligen
A/Reference number: S20483; MUID:92167956; PMID:1538694
A/Accession: S20484
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-169 <VIE>
A/Cross-references: UNIPROT:Q00644; EMBL:X64772; NID:g38684; PIDN:CAA46020.1; PID:g58069;
C/Genetic8;
A/Start codon: GTG

Query Match      48.1%; Score 39; DB 2; Length 169;
Best Local Similarity 57.1%; Pred. No. 35;
Matches      8; Conservative      0; Mismatches      6; Indels      0; Gaps      0;

Qy      2  LGNSSPRTQSPQNC 15
      |||  |||  |||  |||  |||
Db      6  LFNSSPRAGGFSAC 19

RESULT 35
A45056
osteogenic protein 2 precursor - human
N/Alternate names: bone morphogenetic protein 8; OP-2
C/Species: Homo sapiens (man)
C/Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A45056
R/Ozskaynak, E.; Schnegelsberg, P.N.; Jin, D.F.; Clifford, G.M.; Warren, F.D.; Drier, E.;
J. Biol. Chem. 267, 25220-25227, 1992
A/Title: Osteogenic protein-2. A new member of the transforming growth factor-beta super:
A/Reference number: A45056; MUID:93094231; PMID:1460021
A/Accession: A45056
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-402 <OZK>
A/Cross-references: UNIPROT:P34820; GB:M97016; NID:g189389; PIDN:AAB01360.1; PID:g189390
A/Experimental source: hippocampus
A/Note: sequence extracted from NCBI backbone (NCBIP:120189)
C/Genetics;
A/Gene: GDB:EMP8; OP-2
A/Cross-references: GDB:I36392
C/Superfamily: inhibin

Query Match      48.1%; Score 39; DB 2; Length 402;
Best Local Similarity 58.3%; Pred. No. 83;
Matches      7; Conservative      2; Mismatches      3; Indels      0; Gaps      0;

Qy      1  LLGNSSPRTQSP 12
      |||  |||  |||  |||  |||
Db      235  LLGQAPRSQQP 246

RESULT 36
B46165
envelope surface glycoprotein SU - feline leukemia virus (strain FA27)
C/Species: feline leukemia virus
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: B46165
R/Brojatsch, J.; Kristal, B.S.; Viglianti, G.A.; Khirya, R.; Hoover, E.A.; Mullins, J.I
Proc. Natl. Acad. Sci. U.S.A. 89, 8457-8461, 1992
A/Title: Feline leukemia virus subgroup C phenotype evolves through distinct alterations
A/Reference number: A46165; MUID:92409535; PMID:1326757

```

```
A:Accession: B46165
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-403 <BRO>
A:Cross-references: UNIPROT:Q85518; UNIPROT:Q9PXP6; GB:M89998
C:Superfamily: type C retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; spike protein; transmembrane protein

Query Match      48.1%; Score 39; DB 2; Length 403;
Best Local Similarity 46.7%; Pred. No. 84;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLGNSPRTQSPQC 15
Db 293 ILGNSYNQNTNPPSC 307

RESULT 37
C46165
envelope surface glycoprotein SU - feline leukemia virus (strain FS246)
C:Species: feline leukemia virus
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: C46165
R:Brojatsch, J.; Kristal, B.S.; Viglianti, G.A.; Khiraya, R.; Hoover, E.A.; Mullins, J.I
Proc. Natl. Acad. Sci. U.S.A. 89, 8457-8461, 1992
A:Title: Feline leukemia virus subgroup C phenotype evolves through distinct alterations
A:Reference number: A46165; MUID:92409535; PMID:1326757
A:Accession: C46165
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-408 <BRO>
A:Cross-references: UNIPROT:Q02077; GB:M89999
C:Superfamily: type C retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; spike protein; transmembrane protein

Query Match      48.1%; Score 39; DB 2; Length 408;
Best Local Similarity 46.7%; Pred. No. 85;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLGNSPRTQSPQC 15
Db 298 ILGNSYNQNTNPPSC 312

RESULT 38
T16484
hypothetical protein F56D2.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16484
R:Du, Z.
submitted to the EMBL Data Library, August 1994
A:Reference number: Z18519
A:Accession: T16484
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-481 <BUZ>
A:Cross-references: UNIPROT:Q76337; EMBL:U13644; NID:G532100; PID:G1945499; PIDN:AAB5268
A:Experimental source: strain Bristol N2; clone F56D2
C:Genetics:
A:Gene: CESP:F56D2.7
A:Map position: 3
A:Introns: 41/1; 133/3; 230/3; 377/1

Query Match      48.1%; Score 39; DB 2; Length 481;
Best Local Similarity 63.6%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 GNSSPRTQSPQ 13
Db 26 GSSSPSTSAQ 36

RESULT 39
T43064
CED-6 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43064
R:Liu, Q.A.; Hengartner, M.O.
Cell 93, 961-972, 1998
A:Title: Candidate adaptor protein CED-6 promotes the engulfment of apoptotic cells in C. elegans
A:Reference number: 222309; MUID:98297349; PMID:9635426
A:Accession: T43064
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-492 <LIU>
A:Cross-references: UNIPROT:O76337; EMBL:AF061513; NID:G32533307; PIDN:AAC24362.1; PID:G32533307
C:Genetics:
A:Map position: 3
A:Note: ced-6

Query Match      48.1%; Score 39; DB 2; Length 492;
Best Local Similarity 63.6%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 GNSSPRTQSPQ 13
Db 26 GSSSPSTSAQ 36

RESULT 40
S33957
coat protein gamma-COP - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S33957; S27017; S33958
R:Wieland, F.
submitted to the EMBL Data Library, March 1993
A:Reference number: S33957
A:Accession: S33957
A:Molecule type: mRNA
A:Residues: 1-563 <WIR>
A:Cross-references: UNIPROT:P53620; EMBL:X70019; NID:G311340; PIDN:CAA49616.1; PID:G93113
R:Stenbeck, G.; Schreiner, R.; Herrmann, D.; Auerbach, S.; Lottspeich, F.; Rothman, J.E.
PEBS Lett. 314, 195-198, 1992
A:Title: Gamma-COP, a coat subunit of non-clathrin-coated vesicles with homology to Sec2
A:Reference number: S27017; MUID:93093172; PMID:1360908
A:Accession: S27017
A:Molecule type: mRNA
A:Residues: 40-153, 'GPATLPS', 155-156, 'ASSTTAWCWR', 158, 'PR', 159, 163, 'RP', 181-563 <STE>
A:Cross-references: EMBL:S50823
A:Accession: S33958
A:Molecule type: protein
A:Residues: 267-280; 294-307; 485-495; 551-563 <ST2>

Query Match      48.1%; Score 39; DB 2; Length 563;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LLGNSPRTQSP 12
Db 147 LLGQEGPRTSNP 158

RESULT 41
VCMV52
env polyprotein precursor - feline sarcoma virus (strain GA)
N:Contains: coat protein gp70; coat protein p15E
C:Species: feline sarcoma virus
A:Note: host Felis silvestris catus (domestic cat)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 12-Apr-1996
C:Accession: B33741
R:Guilhot, S.; Hampe, A.; D'Auriol, L.; Galibert, F.
Virology 161, 252-258, 1987
```

A;Title: Nucleotide sequence analysis of the LTRs and env genes of SM-FeSV and GA-FeSV.
A;Reference number: A33741; MUID:88044502; PMID:2823466
A;Accession: B33741
A;Molecule type: DNA
A;Residues: 1-642 <GUI>
C;Genetics:
A;Gene: env
C;Superfamily: type C retrovirus env polyprotein
C;Keywords: coat protein; glycoprotein; polyprotein; spike protein; transmembrane protein
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-445/Product: coat protein gp70 #status predicted <GUP>
F;446-642/Product: coat protein p15E #status predicted <GUQ>
F;34,42,57,267,302,307,331,334,374,390,410,578/Binding site: carbohydrate (Asn) (covalent)

Query Match 48.1%; Score 39; DB 1; Length 642;
Best Local Similarity 46.7%; Pred. No. 1.3e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLGNSSPRTQSPQNC 15
:|||||:|:|:
Db 328 ILGNSNQTNPSPC 342

RESULT 42
T10533
env polyprotein precursor - feline leukemia virus (strain FeLV-FAIDS)
N;Contains: env protein gp70; env protein p15E
C;Species: feline leukemia virus
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10533
R;Donahue, P.R.; Hoover, E.A.; Beltz, G.A.; Riedel, N.; Hirsch, V.M.; Overbaugh, J.; Muller, J.; Virol. 62, 722-731, 1988
A;Title: Strong sequence conservation among horizontally transmissible, minimally pathogenic feline leukemia viruses
A;Reference number: Z17078; MUID:88119207; PMID:2828667
A;Accession: T10533
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-642 <DUN>
A;Cross-references: UNIPROT:Q85522; EMBL:M18247; NID:g3233904; PIDN:AAA93093.1; PID:g3233904
C;Superfamily: type C retrovirus env polyprotein

Query Match 48.1%; Score 39; DB 2; Length 642;
Best Local Similarity 46.7%; Pred. No. 1.3e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLGNSSPRTQSPQNC 15
:|||||:|:|:
Db 328 ILGNSNQTNPSPC 342

RESULT 43
VCMVSS
env polyprotein precursor - feline sarcoma virus (strain SM)
N;Contains: coat protein gp70; coat protein p15E
C;Species: feline sarcoma virus
A;Note: host Felis silvestris catus (domestic cat)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 12-Apr-1996
C;Accession: A33741
R;Guilhot, S.; Hampe, A.; D'Auriol, L.; Galibert, F. Virol. 161, 252-258, 1987
A;Title: Nucleotide sequence analysis of the LTRs and env genes of SM-FeSV and GA-FeSV.
A;Reference number: A33741; MUID:88044502; PMID:2823466
A;Accession: A33741
A;Molecule type: DNA
A;Residues: 1-645 <GUI>
C;Genetics:
A;Gene: env
C;Superfamily: type C retrovirus env polyprotein
C;Keywords: coat protein; glycoprotein; polyprotein; spike protein; transmembrane protein
F;1-36/Domain: signal sequence #status predicted <SIG>
F;37-448/Product: coat protein gp70 #status predicted <GUP>
F;449-645/Product: coat protein p15E #status predicted <GUQ>
F;38,46,61,270,305,310,334,337,377,393,413,581/Binding site: carbohydrate (Asn) (covalent)

Query Match 48.1%; Score 39; DB 1; Length 645;
Best Local Similarity 46.7%; Pred. No. 1.3e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LLGNSSPRTQSPQNC 15
:|||||:|:|:
Db 331 ILGNSNQTNPSPC 345

RESULT 44
S05517
lamin - chicken
C;Species: Gallus gallus (chicken)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S05517
R;Peter, M.; Kitten, G.T.; Lehner, C.F.; Vorbuerger, K.; Bailor, S.M.; Maridor, G.; Niggr, J. Mol. Biol. 208, 393-404, 1989
A;Title: Cloning and sequencing of cDNA clones encoding chicken lamins A and B(1) and conformational epitopes of lamin A
A;Reference number: S05517; MUID:90012208; PMID:2795656
A;Accession: S05517
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-657 <PET>
A;Cross-references: UNIPROT:P13648; EMBL:X16879; NID:g63555; PIDN:CAA34762.1; PID:g63556
C;Superfamily: cytoskeletal keratin
C;Keywords: nucleus

Query Match 48.1%; Score 39; DB 2; Length 657;
Best Local Similarity 47.1%; Pred. No. 1.4e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 1 LLGNSSPRTQ--SPQNC 15
:|||||:|:|:
Db 638 VLGGAGFRQAPAPQC 654

RESULT 45
VCWVGF
env polyprotein - feline leukemia virus (strain Gardner-Arnstein)
N;Contains: knob protein gp70; R protein; spike protein p15E
C;Species: feline leukemia virus
A;Note: host Felis sp. (cat)
C;Date: 20-Sep-1984 #sequence_revision 20-Sep-1984 #text_change 09-Jul-2004
C;Accession: A03991
R;Nunberg, J.H.; Williams, M.E.; Innis, M.A. J. Virol. 49, 629-632, 1984
A;Title: Nucleotide sequences of the envelope genes to two isolates of feline leukemia virus
A;Reference number: A92996; MUID:84115095; PMID:6319767
A;Accession: A03991
A;Molecule type: DNA
A;Residues: 1-662 <NUN>
A;Cross-references: UNIPROT:P03391; GB:K01209; NID:g3233910; PIDN:AAA43052.1; PID:g3233911
R;Elder, J.H.; McGee, J.S.; Munson, M.; Houghten, R.A.; Kloetzer, W.; Bittle, J.L.; Grant, J. Virol. 61, 8-15, 1987
A;Title: Localization of neutralizing regions of the envelope gene of feline leukemia virus
A;Reference number: A25982; MUID:87061257; PMID:2431166
A;Contents: annotation; peptide synthesis
A;Note: 27 peptides synthesized
C;Genetics:
A;Gene: env
C;Superfamily: type C retrovirus env polyprotein
C;Keywords: coat protein; glycoprotein; polyprotein; spike protein; transmembrane protein
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-465/Product: knob protein gp70 #status predicted <KPG>
F;466-645/Product: spike protein p15E #status predicted <SKP>
F;646-662/Product: R protein #status predicted <RRP>
F;43,58,286,322,327,351,354,394,410,430/Binding site: carbohydrate (Asn) (covalent) #stat

Query Match 48.1%; Score 39; DB 1; Length 662;
Best Local Similarity 46.7%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 842 IGNSNHGSQSPRN 854

Search completed: August 25, 2005, 11:44:35
Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2005, 11:38:14 ; Search time 161 Seconds
(without alignments)

36.608 Million cell updates/sec

Title: US-10-803-541-2

Perfect score: 81

Sequence: 1 LLGNSSPRQSPQNC 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1767149 seqs, 392926209 residues

Total number of hits satisfying chosen parameters: 1767149

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	81	100.0	15	17	US-10-803-541-2
2	81	100.0	18	17	US-10-803-541-20
3	81	100.0	515	10	US-09-315-355-46
4	81	100.0	515	18	US-10-848-572-46
5	81	100.0	664	16	US-10-408-765A-2079
6	81	100.0	664	16	US-10-473-127-1658
7	81	100.0	664	17	US-10-943-400-2
8	81	100.0	664	17	US-10-803-541-4
9	69	85.2	15	17	US-10-803-541-16
10	69	85.2	18	17	US-10-803-541-21
11	69	85.2	665	17	US-10-803-541-9

Sequence 132511,	16	55.6	162	16	US-10-437-963-132511	Sequence 132511,
Sequence 198650,	16	54.3	122	16	US-10-425-115-198650	Sequence 198650,
Sequence 145179,	16	54.3	275	15	US-10-424-599-145179	Sequence 145179,
Sequence 2862, Ap	15	54.3	286	15	US-10-094-749-2862	Sequence 2862, Ap
Sequence 117902,	16	54.3	826	16	US-10-437-963-117902	Sequence 117902,
Sequence 202808,	17	53.1	539	16	US-10-437-963-202808	Sequence 202808,
Sequence 392, App	18	53.1	558	18	US-10-481-032A-392	Sequence 392, App
Sequence 203613,	19	53.1	1797	16	US-10-437-963-203613	Sequence 203613,
Sequence 203615,	20	53.1	2001	16	US-10-437-963-203615	Sequence 203615,
Sequence 46748, A	21	52.5	202	16	US-10-767-701-46748	Sequence 46748, A
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Sequence 324347,	22	51.9	100	16	US-10-425-115-324347	Sequence 324347,
Sequence 20, Appl	23	51.9	175	15	US-10-283-940-20	Sequence 20, Appl
Sequence 19, Appl	25	51.9	175	20	US-11-022-454-19	Sequence 19, Appl
Sequence 19, Appl	26	51.9	177	10	US-09-994-064-19	Sequence 19, Appl
Sequence 19, Appl	27	51.9	177	11	US-09-993-777-19	Sequence 19, Appl
Sequence 206208,	28	51.9	177	11	US-10-836-383-19	Sequence 206208,
Sequence 3255, Ap	29	51.9	183	15	US-10-424-599-206208	Sequence 3255, Ap
Sequence 203609,	30	51.9	256	15	US-10-104-047-3255	Sequence 203609,
Sequence 204611,	31	51.9	1701	16	US-10-437-963-203609	Sequence 204611,
Sequence 203618,	32	51.9	1828	16	US-10-437-963-204611	Sequence 203618,
Sequence 17, Appl	33	51.9	1980	16	US-10-437-963-203618	Sequence 17, Appl
Sequence 218829,	34	51.9	2150	13	US-10-135-322-17	Sequence 218829,
Sequence 352933,	35	50.6	78	16	US-10-425-115-218829	Sequence 352933,
Sequence 230506,	36	50.6	86	16	US-10-425-115-230506	Sequence 230506,
Sequence 57287, A	37	50.6	112	15	US-10-424-599-230506	Sequence 57287, A
Sequence 38640, A	38	50.6	112	16	US-10-767-701-57287	Sequence 38640, A
Sequence 47848, A	39	50.6	243	15	US-10-425-114-38640	Sequence 47848, A
Sequence 60855, A	40	50.6	310	15	US-10-425-114-47848	Sequence 60855, A
Sequence 69314, A	41	50.6	316	15	US-10-425-114-60855	Sequence 69314, A
Sequence 257256,	42	50.6	320	15	US-10-425-114-69314	Sequence 257256,
Sequence 258656,	43	50.6	328	16	US-10-425-115-257256	Sequence 258656,
Sequence 258661,	44	50.6	334	16	US-10-425-115-258661	Sequence 258661,
Sequence 257255,	45	50.6	338	16	US-10-425-115-258661	Sequence 257255,
Sequence 58835, A	46	50.6	343	16	US-10-425-115-257255	Sequence 58835, A
Sequence 258659, A	47	50.6	354	16	US-10-425-114-58835	Sequence 258659, A
Sequence 60636, A	48	50.6	364	16	US-10-425-115-258659	Sequence 60636, A
Sequence 59471, A	49	50.6	365	15	US-10-425-114-60636	Sequence 59471, A
Sequence 67675, A	50	50.6	370	15	US-10-425-114-67675	Sequence 67675, A
Sequence 67309, A	51	50.6	370	15	US-10-425-114-67309	Sequence 67309, A
Sequence 189698,	52	50.6	378	15	US-10-425-114-67309	Sequence 189698,
Sequence 1261, Ap	53	50.0	100	15	US-10-424-599-189698	Sequence 1261, Ap
Sequence 7568, Ap	54	49.4	10	18	US-10-862-195-1261	Sequence 7568, Ap
Sequence 351554,	55	49.4	54	14	US-10-156-761-7568	Sequence 351554,
Sequence 297429,	56	49.4	81	16	US-10-425-115-351554	Sequence 297429,
Sequence 269275,	57	49.4	104	16	US-10-425-115-297429	Sequence 269275,
Sequence 284701,	58	49.4	120	15	US-10-424-599-269275	Sequence 284701,
Sequence 4841, Ap	59	49.4	123	16	US-10-425-115-284701	Sequence 4841, Ap
Sequence 54437, A	60	49.4	170	15	US-10-108-260A-4841	Sequence 54437, A
Sequence 233052,	61	49.4	197	16	US-10-767-701-54437	Sequence 233052,
Sequence 3520, Ap	62	49.4	226	16	US-10-425-115-233052	Sequence 3520, Ap
Sequence 63508, A	63	49.4	234	15	US-10-108-260A-3520	Sequence 63508, A
Sequence 1615, Ap	64	49.4	491	15	US-10-425-114-63508	Sequence 1615, Ap
Sequence 2149, Ap	65	49.4	713	16	US-10-408-765A-1615	Sequence 2149, Ap
Sequence 200705,	66	49.4	828	16	US-10-408-765A-2149	Sequence 200705,
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Sequence 5791, Ap	70	49.4	1020	18	US-10-712-124-122	Sequence 5791, Ap
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Sequence -807, App	72	49.4	1048	18	US-10-322-281-810	Sequence -807, App
Sequence 169, App	73	49.4	2053	16	US-10-322-281-807	Sequence 169, App
Sequence 11, Appl	74	49.4	4823	15	US-10-051-874-169	Sequence 11, Appl
Sequence 8, Appli	75	48.8	5877	14	US-10-142-515-11	Sequence 8, Appli
Sequence 5, Appli	76	48.8	5935	14	US-10-243-443A-8	Sequence 5, Appli
Sequence 17, Appl	77	48.8	22152	16	US-10-715-066-5	Sequence 17, Appl
Sequence 22, Appl	78	48.1	39	17	US-10-803-541-17	Sequence 22, Appl
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Sequence 278007,	80	48.1	45	14	US-10-029-386-30358	Sequence 278007,
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; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: US 08/705,660
; PRIOR FILING DATE: 1996-08-30
; PRIOR APPLICATION NUMBER: US 09/315,355
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-848-572-46

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Best Local Similarity 100.0%; Pred. No. 0.00041;
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Db 498 LLGNSPRTQSPQNC 512

RESULT 5
US-10-408-765A-2079
; Sequence 2079, Application US/10408765A
; Publication No. US20040101974A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2079
; LENGTH: 664
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2079

Query Match 100.0%; Score 81; DB 16; Length 664;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLGNSPRTQSPQNC 15
Db 647 LLGNSPRTQSPQNC 661

RESULT 6
US-10-473-127-1658
; Sequence 1658, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370

; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1658
; LENGTH: 664
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1658

Query Match 100.0%; Score 81; DB 16; Length 664;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLGNSPRTQSPQNC 15
Db 647 LLGNSPRTQSPQNC 661

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; Sequence 2, Application US/10943400
; Publication No. US20050059071A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services
; APPLICANT: Eriksson, B. Maria H.
; APPLICANT: Collins, Francis S.
; APPLICANT: Gordon, Leslie B.
; APPLICANT: Brown, W. Ted
; TITLE OF INVENTION: LMNA GENE AND ITS INVOLVEMENT IN HUTCHINSON-GILFORD PROGERIA
; TITLE OF INVENTION: SYNDROME (HGPS) AND ARTERIOSCLEROSIS
; FILE REFERENCE: 4239-66648-02
; CURRENT APPLICATION NUMBER: US/10/943,400
; CURRENT FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: US 60/419,541
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: PCT/US2003/0033058
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US 60/463,084
; PRIOR FILING DATE: 2002-04-14
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 664
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-943-400-2

Query Match 100.0%; Score 81; DB 17; Length 664;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLGNSPRTQSPQNC 15
Db 647 LLGNSPRTQSPQNC 661

RESULT 8
US-10-803-541-4
; Sequence 4, Application US/10803541
; Publication No. US20050090438A1
; GENERAL INFORMATION:
; APPLICANT: Brodey, Gary
; TITLE OF INVENTION: Product and Methods for Diagnosis and Therapy for Cardiac and
; TITLE OF INVENTION: Skeletal Muscle Disorders
; FILE REFERENCE: 2848-53
; CURRENT APPLICATION NUMBER: US/10/803,541
; CURRENT FILING DATE: 2004-03-17

; PRIOR APPLICATION NUMBER: 60/456,642
; PRIOR FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4
; LENGTH: 664
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-803-541-4

Query Match 100.0%; Score 81; DB 17; Length 664;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSPQNC 15
Db 647 LLGNSSPRTQSPQNC 661

RESULT 9

US-10-803-541-16
; Sequence 16, Application US/10803541
; Publication No. US2005090438A1
; GENERAL INFORMATION:
; APPLICANT: Brodsky, Gary
; TITLE OF INVENTION: Product and Methods for Diagnosis and Therapy for Cardiac and
; FILE REFERENCE: 2848-53
; CURRENT APPLICATION NUMBER: US/10/803,541
; CURRENT FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: 60/456,642
; PRIOR FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-803-541-16

Query Match 85.2%; Score 69; DB 17; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.00082;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSPQNC 15
Db 1 LLGNSSPRSQSQNC 15

RESULT 10

US-10-803-541-21
; Sequence 21, Application US/10803541
; Publication No. US2005090438A1
; GENERAL INFORMATION:
; APPLICANT: Brodsky, Gary
; TITLE OF INVENTION: Product and Methods for Diagnosis and Therapy for Cardiac and
; FILE REFERENCE: 2848-53
; CURRENT APPLICATION NUMBER: US/10/803,541
; CURRENT FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: 60/456,642
; PRIOR FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 21
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-803-541-21

Query Match 85.2%; Score 69; DB 17; Length 18;
Best Local Similarity 86.7%; Pred. No. 0.00098;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSPQNC 15
Db 1 LLGNSSPRSQSQNC 15

RESULT 11

US-10-803-541-9
; Sequence 9, Application US/10803541
; Publication No. US2005090438A1
; GENERAL INFORMATION:
; APPLICANT: Brodsky, Gary
; TITLE OF INVENTION: Product and Methods for Diagnosis and Therapy for Cardiac and
; FILE REFERENCE: 2848-53
; CURRENT APPLICATION NUMBER: US/10/803,541
; CURRENT FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: 60/456,642
; PRIOR FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 9
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-803-541-9

Query Match 85.2%; Score 69; DB 17; Length 665;
Best Local Similarity 86.7%; Pred. No. 0.038;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSPQNC 15
Db 648 LLGNSSPRSQSQNC 662

RESULT 12

US-10-437-963-132511
; Sequence 132511, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 132511
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_34473C.1.pap
US-10-437-963-132511

Query Match 55.8%; Score 45; DB 16; Length 162;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSPQNC 15
Db 93 LLGNSSPSSGEOCC 107

RESULT 13

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US-10-425-115-198650
; Sequence 198650, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 198650
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_112748C.1.pep
US-10-425-115-198650

Query Match      54.3%; Score 44; DB 16; Length 122;
Best Local Similarity 72.7%; Pred. No. 52;
Matches      8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2 LGNSSPRTQSP 12
Db      62 LGSSAPRTQPP 72
|||:|||||
|||:|||||

RESULT 14
US-10-424-599-145179
; Sequence 145179, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 145179
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_102114C.1.pep
US-10-424-599-145179

Query Match      54.3%; Score 44; DB 15; Length 275;
Best Local Similarity 61.5%; Pred. No. 1.2e+02;
Matches      8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      2 LGNSSPRTQSPON 14
Db      4 LGNEQPGTQIPEN 16
|||:|||||
|||:|||||

RESULT 15
US-10-094-749-2862
; Sequence 2862, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
```

```
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2862
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2862

Query Match      54.3%; Score 44; DB 15; Length 286;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches      8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      6 SPRTQSPQNC 15
Db      71 SPRTQSPGCG 80
|||||||
|||||||

RESULT 16
US-10-437-963-117902
; Sequence 117902, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 117902
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_21264C.1.pep
US-10-437-963-117902

Query Match      54.3%; Score 44; DB 16; Length 826;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches      8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 LLGNSSPRTQSP 12
Db      403 LLGNEGPRTSDP 414
|||||||
|||||||
```

```
RESULT 17
US-10-437-963-202808
; Sequence 202808, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 202808
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_98052C.1.pep
US-10-437-963-202808

Query Match      53.1%; Score 43; DB 16; Length 539;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches      8; Conservative      1; Mismatches      3; Indels      0; Gaps      0;

QY      1  LLGNSSPRTQSP 12
      :||| |||||
DB      409  LVGNSPRTTP 420

RESULT 18
US-10-481-032A-392
; Sequence 392, Application US/10481032A
; Publication No. US20050177901A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Cheng, Wengqiong
; APPLICANT: Briggs, Steven
; APPLICANT: Cooper, Bret
; APPLICANT: Goff, Stephen A.
; APPLICANT: Moughamer, Todd
; APPLICANT: Glazebrook, Jane
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicolas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 60148USPCT
; CURRENT APPLICATION NUMBER: US/10/481,032A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/300,112
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/342,327
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/IB02/02450
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 1201
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 392
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-481-032A-392
```

```
Query Match      53.1%; Score 43; DB 18; Length 558;
Best Local Similarity 57.1%; Pred. No. 3.5e+02;
Matches      8; Conservative      3; Mismatches      3; Indels      0; Gaps      0;

QY      1  LLGNSSPRTQSPON 14
      :||| |||||
DB      231  ILQSNIPRTQPPQN 244

RESULT 19
US-10-437-963-203613
; Sequence 203613, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 203613
; LENGTH: 1797
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1797)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_98780C.1.pep
US-10-437-963-203613

Query Match      53.1%; Score 43; DB 16; Length 1797;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches      8; Conservative      3; Mismatches      3; Indels      0; Gaps      0;

QY      1  LLGNSSPRTQSPON 14
      :||| |||||
DB      210  ILQSNIPRTQPPQN 223

RESULT 20
US-10-437-963-203615
; Sequence 203615, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 203615
; LENGTH: 2001
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
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OTHER INFORMATION: Clone ID: PAT_MRT4530_98782C.1.pep
US-10-437-963-203615

Query Match 53.1%; Score 43; DB 16; Length 2001;
Best Local Similarity 57.1%; Pred. No. 1.3e+03;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSPQN 14
Db 231 ILQSNIPRTQPPQN 244

RESULT 21

US-10-767-701-46748
; Sequence 46748, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46748
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C49_82.pep
US-10-767-701-46748

Query Match 52.5%; Score 42.5; DB 16; Length 202;
Best Local Similarity 69.2%; Pred. No. 1.5e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 3 GNSSPRTQSPQNC 15
Db 154 GNISPLTQ-PENC 165

RESULT 22

US-10-424-599-234564
; Sequence 234564, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 234564
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_53839C.1.pep
US-10-424-599-234564

Query Match 51.9%; Score 42; DB 15; Length 81;
Best Local Similarity 46.7%; Pred. No. 70;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSPQNC 15
Db 24 LCGAPPRTSPRC 38

RESULT 23

US-10-425-115-324347
; Sequence 324347, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 324347
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_58879C.1.pep
US-10-425-115-324347

Query Match 51.9%; Score 42; DB 16; Length 100;
Best Local Similarity 61.5%; Pred. No. 87;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSPQ 13
Db 54 LVGNSSPNLGTGPQ 66

RESULT 24

US-10-283-940-20
; Sequence 20, Application US/10283940
; Publication No. US20030220394A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Morgan, Andrew J
; APPLICANT: Yu, Shukun
; APPLICANT: Weiergang, Inge
; APPLICANT: Pedersen, Hans C
; TITLE OF INVENTION: Sequences
; FILE REFERENCE: 674509-2041.1
; CURRENT APPLICATION NUMBER: US/10/283,940
; CURRENT FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: PCT/GB02/04916
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: GB 0126164.3
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/343,485
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Phanerochaete chrysosporium
US-10-283-940-20

Query Match 51.9%; Score 42; DB 15; Length 175;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 LGNSSPRTQSPQNC 15
Db 67 IGLGSPITETQRC 80

RESULT 25

US-11-022-454-20

```
; Sequence 20, Application US/11022454
; Publication No. US20050164259A1
; GENERAL INFORMATION:
; APPLICANT: Morgan, Andrew John Pedersen, Hans Christian
; APPLICANT: Weiergang, Inge
; APPLICANT: Yu, Shukun
; TITLE OF INVENTION: Sequences
; FILE REFERENCE: 674509-2041.2
; CURRENT APPLICATION NUMBER: US/11/022,454
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 10/283,940
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: PCT/GB02/04916
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: GB 0126164.3
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/343,485
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Phanerochaete chrysosporium
; US-11-022-454-20

Query Match 51.9%; Score 42; DB 20; Length 175;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 LGNSSPRTQSPQNC 15
Db 67 IGLGSPITETPQRC 80

RESULT 26
US-09-994-064-19
; Sequence 19, Application US/09994064
; Publication No. US20030082789A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Martha A.
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/994,064
; FILING DATE: 08/04/2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,190
; FILING DATE: 23-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,597
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39116-A
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-994-064-19

Query Match 51.9%; Score 42; DB 11; Length 177;
Best Local Similarity 53.3%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSPQNC 15
Db 5 LLNRGSPRLNSPPKC 19

RESULT 28
US-10-836-383-19
```

```
; LENGTH: 177 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-994-064-19

Query Match 51.9%; Score 42; DB 10; Length 177;
Best Local Similarity 53.3%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSPQNC 15
Db 5 LLNRGSPRLNSPPKC 19

RESULT 27
US-09-993-777-19
; Sequence 19, Application US/09993777
; Publication No. US20040171132A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Martha A.
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/993,777
; FILING DATE: 06-NOV-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,190C
; FILING DATE: 23-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,597
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39116-A
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-993-777-19

Query Match 51.9%; Score 42; DB 11; Length 177;
Best Local Similarity 53.3%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 LLGNSSPRTQSPQNC 15
Db 5 LLNRGSPRLNSPPKC 19

RESULT 28
US-10-836-383-19
```

; Sequence 19, Application US/10836383
; Publication No. US20040228878A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Martha A.
; COCHRAN, Mark D.
; TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
; AND USES THEREOF
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/836,383
; FILING DATE: 30-Apr-2004
; CLASSIFICATION DATA:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,190C
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/126,597
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39116-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-836-383-19
Query Match 51.9%; Score 42; DB 16; Length 177;
Best Local Similarity 53.3%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 LLGNSPRTQSPQNC 15
DB 5 LLNRGSPRLNSPPKC 19
RESULT 29
US-10-424-599-206208
; Sequence 206208, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 206208
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Glycine max

; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_28232C.1.pep
US-10-424-599-206208
Query Match 51.9%; Score 42; DB 15; Length 183;
Best Local Similarity 72.7%; Pred. No. 1.6e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 4 NSSPRTQSPQN 14
DB 51 NSNPQAQSPQN 61
RESULT 30
US-10-104-047-3255
; Sequence 3255, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3255
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3255
Query Match 51.9%; Score 42; DB 15; Length 256;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 GNSPRTQSP 12
DB 234 GNSPHTASP 243
RESULT 31
US-10-437-963-203609
; Sequence 203609, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 203609
; LENGTH: 1701
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_98777C.1.pep
US-10-437-963-203609
Query Match 51.9%; Score 42; DB 16; Length 1701;
Best Local Similarity 57.1%; Pred. No. 1.5e+03;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```
Qy 1 LLGSSPRTQSPQN 14
    :|::|||
Db 210 ILQSNIPRTQLPQN 223

RESULT 32
US-10-437-963-204611
; Sequence 204611, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 204611
; LENGTH: 1828
; TYPE: PRT
; ORGANISM: Oryza sativa
; NAME/KEY: unsure
; LOCATION: (1)..(1828)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_99681C.1.pep
US-10-437-963-204611

Query Match 51.9%; Score 42; DB 16; Length 1828;
Best Local Similarity 57.1%; Pred. No. 1.7e+03;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGSSPRTQSPQN 14
    :|::|||
Db 210 ILQSNIPRTQLPQN 223

RESULT 33
US-10-437-963-203618
; Sequence 203618, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 203618
; LENGTH: 1980
; TYPE: PRT
; ORGANISM: Oryza sativa
; NAME/KEY: unsure
; LOCATION: (1)..(1980)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
```

```
; OTHER INFORMATION: Clone ID: PAT_MRT4530_98785C.1.pep
US-10-437-963-203618

Query Match 51.9%; Score 42; DB 16; Length 1980;
Best Local Similarity 57.1%; Pred. No. 1.8e+03;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLGSSPRTQSPQN 14
    :|::|||
Db 231 ILQSNIPRTQLPQN 244

RESULT 34
US-10-135-322-17
; Sequence 17, Application US/10135322
; Publication No. US20020173017A1
; GENERAL INFORMATION:
; APPLICANT: BENFEY, PN
; APPLICANT: HELARIUTTA, Y
; APPLICANT: MAHONEN, AP
; APPLICANT: BONKE, AMN
; APPLICANT: KAUPPINEN, L
; APPLICANT: RIIKONEN, M
; TITLE OF INVENTION: WOODEN LEG GENE, PROMOTER AND USES THEREOF
; FILE REFERENCE: 5914-086-999
; CURRENT APPLICATION NUMBER: US/10/135,322
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/253,739
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 2150
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-135-322-17

Query Match 51.9%; Score 42; DB 13; Length 2150;
Best Local Similarity 53.8%; Pred. No. 2e+03;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GNSPRTQSPQNC 15
    ||::||
Db 345 GNSPRTQSPQNC 357

RESULT 35
US-10-425-115-218829
; Sequence 218829, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 218829
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_131163C.1.pep
US-10-425-115-218829

Query Match 50.6%; Score 41; DB 16; Length 78;
Best Local Similarity 70.0%; Pred. No. 96;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```



```
Qy 6 SPRTSQPQNC 15
Db 22 SPMTQSPRC 31

RESULT 36
US-10-425-115-252593
; Sequence 252593, Application US/10425115
; Publication No. US2004021472A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 252593
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_161948C.1.pep
US-10-425-115-252593

Query Match 50.6%; Score 41; DB 16; Length 86;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Qy 3 GNSSPR--TQSPQNC 15
Db 15 GVSQPRVCTQAPMNC 29

RESULT 37
US-10-424-599-230506
; Sequence 230506, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 230506
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_50169C.1.pep
US-10-424-599-230506

Query Match 50.6%; Score 41; DB 15; Length 112;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 SSPTQSPQNC 15
Db 55 STPRSSDDQNC 65

RESULT 38
US-10-767-701-57287
; Sequence 57287, Application US/10767701
; Publication No. US20040172684A1

; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 57287
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 30965256.pep
US-10-767-701-57287

Query Match 50.6%; Score 41; DB 16; Length 112;
Best Local Similarity 58.3%; Pred. No. 1.4e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GNSSPRTQSPON 14
Db 1 GSRSPRSRSPQD 12

RESULT 39
US-10-425-114-38640
; Sequence 38640, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 38640
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700347220_FLI.pep
US-10-425-114-38640

Query Match 50.6%; Score 41; DB 15; Length 243;
Best Local Similarity 58.3%; Pred. No. 3.1e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GNSSPRTQSPON 14
Db 118 GSRSPRSRSPQD 129

RESULT 40
US-10-425-114-47848
; Sequence 47848, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
```

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 47848
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700267149_FLI.pep
US-10-425-114-47848

Query Match 50.6%; Score 41; DB 15; Length 310;
Best Local Similarity 58.3%; Pred. No. 3.9e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GNSSPRTQSPON 14
|:|:|:|:|:
Db 199 GSRSPRSRSPQD 210

RESULT 41

US-10-425-114-60855
; Sequence 60855, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 60855
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3354-031-A12_FLI.pep
US-10-425-114-60855

Query Match 50.6%; Score 41; DB 15; Length 316;
Best Local Similarity 58.3%; Pred. No. 4e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GNSSPRTQSPON 14
|:|:|:|:|:
Db 211 GSRSPRSRSPQD 222

RESULT 42

US-10-425-114-69314
; Sequence 69314, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 69314
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZWFLM017123H02_FLI.pep
US-10-425-114-69314

Query Match 50.6%; Score 41; DB 15; Length 320;
Best Local Similarity 58.3%; Pred. No. 4e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GNSSPRTQSPON 14
|:|:|:|:|:
Db 195 GSRSPRSRSPQD 206

RESULT 43

US-10-425-115-257256
; Sequence 257256, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 257256
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_166202C.1.pep
US-10-425-115-257256

Query Match 50.6%; Score 41; DB 16; Length 328;
Best Local Similarity 58.3%; Pred. No. 4.1e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GNSSPRTQSPON 14
|:|:|:|:|:
Db 203 GSRSPRSRSPQD 214

RESULT 44

US-10-425-115-258656
; Sequence 258656, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 258656
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_167481C.1.pep
US-10-425-115-258656

Query Match 50.6%; Score 41; DB 16; Length 334;

Best Local Similarity 58.3%; Pred. No. 4.2e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 GNSSPRTQSPQN 14
| : | | | : | | :
db 228 GSRSPRRSRSPD 239

```

RESULT 45
US-10-425-115-258661
  Sequence 258661, Application US/10425115
  Publication No. US20040214272A1
  GENERAL INFORMATION:
  APPLICANT: La Rosa, Thomas J.
  APPLICANT: Kovalic, David K.
  APPLICANT: Zhou, Yihua
  APPLICANT: Cao, Yongwei
  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
  TITLE OF INVENTION: Plants
  FILE REFERENCE: 38-21(53222)B
  CURRENT APPLICATION NUMBER: US/10/425,115
  CURRENT FILING DATE: 2003-04-28
  NUMBER OF SEQ ID NOS: 369326
  SEQ ID NO 258661
  LENGTH: 338
  TYPE: PRT
  ORGANISM: Zea mays
  FEATURE:
  NAME/KEY: unsure
  LOCATION: (1)..(338)
  OTHER INFORMATION: unsure at all Xaa locations
  FEATURE:
  OTHER INFORMATION: Clone ID: MFT4577_167486C.1.pep
US-10-425-115-258661

```

Query Match 50.6%; Score 41; DB 16; Length 338;
Best Local Similarity 58.3%; Pred. No. 4.3e+02;
Matches 7: Conservative 4; Mismatches 1; Indels

Qy 3 GNSSPRTQSPQN 14
|: |||::|||:
pb 235 GSRSPRRSRSPOD 246

```

RESULT 46
US-10-425-115-257255
; Sequence 257255, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: Thomas J.
; APPLICANT: La Rosa, David K.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 257255
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_166201C.1.pep
US-10-425-115-257255

```

Query Match 50.6%; Score 41; DB 16; Length 343;
Best Local Similarity 58.3%; Pred. No. 4.3e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 GNSSPRTQSPQN 14
| : ||| : ||| :
| : ||| : ||| :

db 228 GSRSPRSPD 239

RESULT 47

```

US-10-425-114-58835
; Sequence 58835, Application US/10425114
; Publication NO. US20040034888A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 58835
; LENGTH: 354
; TYPE: ERT
; ORGANISM: Zea mays
;
; FEATURES:
;
; OTHER INFORMATION: Clone ID: 700221865_FLI.pep
US-10-425-114-58835

```

Query Match 50.6%; Score 41; DB 15; Length 354;
Best Local Similarity 58.3%; Pred. No. 4.5e+02;
Matches 7; Conservative 4; Mismatches 1; Indels

Qy 3 GNSSPRTQSPQN 14
| : | | | : | | :
Db 229 GSRSPRRSRSPOD 24

```

RESULT 48
US-10-425-115-258659
; Sequence 258659, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 258659
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MET4577_l67484C.1.pep
US-10-425-115-258659

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Query Match 50.6%; Score 41; DB 16; Length 364;
Best Local Similarity 58.3%; Pred. No. 4.6e+02;
Matches 7: Conservative 4; Mismatches 1; Indels

Qy 3 GNSSPRTQSPQN 14
| : | | : | | : |
Db 228 GSRSPRSPQD 239

RESULT 49
US-10-425-114-60636
; Sequence 60636, Application US/10425114
; Publication No. US20040034888A1

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; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 60636
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3356-001-A11_FLI.pep
US-10-425-114-60636

Query Match          50.6%; Score 41; DB 15; Length 365;
Best Local Similarity 58.3%; Pred. No. 4.6e+02;
Matches      7; Conservative    4; Mismatches   1; Indels    0; Gaps    0;

QY       3 GNSSPRTSQSPON 14
| : | | | : | | | :
Db        262 GSRSPRSRSPD 273

RESULT 50
US-10-425-114-59471
; Sequence 59471, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59471
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3151-024-C2_FLI.pep
US-10-425-114-59471

Query Match          50.6%; Score 41; DB 15; Length 370;
Best Local Similarity 58.3%; Pred. No. 4.7e+02;
Matches      7; Conservative    4; Mismatches   1; Indels    0; Gaps    0;

QY       3 GNSSPRTSQSPON 14
| : | | | : | | | :
Db        255 GSRSPRSRSPD 266

Search completed: August 25, 2005, 11:48:10
Job time : 163 secs
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